

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 6, 2004, 12:41:36 ; Search time 39 Seconds  
(without alignments)  
186.075 Million cell updates/sec

Title: US-10-612-885a-1  
Perfect score: 117  
Sequence: 1 ORVEILEGRTECVLSNLRGRTRY 23

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues  
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacterioplasmid:\*  
17: sp\_archaeoplasmid:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 109   | 93.2        | 316    | 11    | O35545      |
| 2          | 107   | 91.5        | 509    | 6     | O9MY29      |
| 3          | 104   | 88.9        | 229    | 6     | O28206      |
| 4          | 104   | 88.9        | 229    | 6     | O27950      |
| 5          | 104   | 88.9        | 387    | 6     | O95N13      |
| 6          | 104   | 88.9        | 418    | 6     | O95N14      |
| 7          | 56    | 47.9        | 176    | 17    | O8TYF5      |
| 8          | 52    | 44.4        | 1028   | 4     | O9UQ52      |
| 9          | 49    | 41.9        | 826    | 2     | O9AKX8      |
| 10         | 48    | 41.9        | 1028   | 11    | P97528      |
| 11         | 48    | 41.0        | 428    | 11    | O9LPY7      |
| 12         | 48    | 41.0        | 1028   | 11    | O9UW88      |
| 13         | 48    | 41.0        | 1028   | 11    | O8C6X1      |
| 14         | 47    | 40.2        | 539    | 10    | O94LS6      |
| 15         | 47    | 40.2        | 539    | 10    | O7XDN4      |
| 16         | 47    | 40.2        | 640    | 10    | O9ASX3      |

|    |      |      |      |    |        |                               |
|----|------|------|------|----|--------|-------------------------------|
| 17 | 47   | 40.2 | 644  | 10 | O8LDV1 | Q8LDV1 arabidopsis            |
| 18 | 47   | 40.2 | 644  | 10 | O9FNK3 | Q9FNK3 arabidopsis            |
| 19 | 47   | 40.2 | 1226 | 16 | O7UJ12 | Q7UJ12 rhodospirillum rubrum  |
| 20 | 47   | 40.2 | 1873 | 10 | O9FC11 | Q9FC11 arabidopsis            |
| 21 | 46   | 39.3 | 288  | 12 | O9E214 | Q9E214 molluscum              |
| 22 | 46   | 39.3 | 637  | 5  | O86G09 | Q86G09 dictyostelium          |
| 23 | 46   | 39.3 | 700  | 11 | O9CXF5 | Q9CXF5 mus musculus           |
| 24 | 46   | 39.3 | 700  | 11 | O8C0B3 | Q8C0B3 mus musculus           |
| 25 | 46   | 39.3 | 781  | 15 | O82857 | Q82857 jembrana di            |
| 26 | 46   | 39.3 | 1283 | 5  | O8TA82 | Q8TA82 caenorhabditis elegans |
| 27 | 45.5 | 38.9 | 95   | 3  | O8TF83 | Q8TF83 agrocorybe             |
| 28 | 45   | 38.5 | 76   | 7  | O30734 | Q30734 macaca fusc            |
| 29 | 45   | 38.5 | 76   | 7  | O30567 | Q30567 macaca fusc            |
| 30 | 45   | 38.5 | 81   | 7  | O30747 | Q30747 macaca fusc            |
| 31 | 45   | 38.5 | 316  | 16 | O912J3 | Q912J3 pseudomonas            |
| 32 | 45   | 38.5 | 446  | 10 | O94CT7 | Q94CT7 oryza sativ            |
| 33 | 45   | 38.5 | 479  | 5  | O9U7P5 | Q9U7P5 eufoillia              |
| 34 | 45   | 38.5 | 567  | 5  | O9VCA3 | Q9VCA3 drosophila             |
| 35 | 45   | 38.5 | 567  | 5  | O9VCA3 | Q9VCA3 drosophila             |
| 36 | 45   | 38.5 | 773  | 16 | O8A0C0 | Q8A0C0 bacteroides            |
| 37 | 45   | 38.5 | 968  | 5  | O7YZ47 | Q7YZ47 cryptospori            |
| 38 | 45   | 38.5 | 1056 | 12 | O57161 | Q57161 spinach lat            |
| 39 | 44.5 | 38.0 | 691  | 5  | O9VW11 | Q9VW11 drosophila             |
| 40 | 44.5 | 38.0 | 693  | 5  | O96680 | Q96680 drosophila             |
| 41 | 44.5 | 38.0 | 810  | 10 | O92W13 | Q92W13 cucurbita m            |
| 42 | 44   | 37.6 | 147  | 16 | O8XFL2 | Q8XFL2 salmone                |
| 43 | 44   | 37.6 | 195  | 16 | O8Z0G3 | Q8Z0G3 anabaena sp            |
| 44 | 44   | 37.6 | 606  | 5  | O9WR6  | Q9WR6 drosophila              |
| 45 | 44   | 37.6 | 2023 | 12 | O91632 | Q91632 cherry gree            |

## ALIGNMENTS

|          |  |       |             |        |       |             |
|----------|--|-------|-------------|--------|-------|-------------|
| RESULT 1 | ID   | Score | Query Match | Length | DB ID | Description |
| O35545   | O35545   | 93.2  | 91.5        | 316    | 11    | O35545      |
| AC       | O35545   | 93.2  | 91.5        | 316    | 11    | O35545      |
| DT       | O1-JAN-1998  | 93.2  | 91.5        | 316    | 11    | O35545      |
| DT       | O1-JAN-1998  | 93.2  | 91.5        | 316    | 11    | O35545      |
| DT       | O1-OCT-2003  | 93.2  | 91.5        | 316    | 11    | O35545      |
| DE       | Intron 5-Inserted form of erythropoietin receptor precursor.             | 93.2  | 91.5        | 316    | 11    | O35545      |
| OS       | Rattus norvegicus (Rat).   | 93.2  | 91.5        | 316    | 11    | O35545      |
| OC       | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;        | 93.2  | 91.5        | 316    | 11    | O35545      |
| OC       | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.    | 93.2  | 91.5        | 316    | 11    | O35545      |
| OX       | NCBI_TaxID=10116;  | 93.2  | 91.5        | 316    | 11    | O35545      |
| RP       | SEQUENCE FROM N.A.   | 93.2  | 91.5        | 316    | 11    | O35545      |
| RX       | MEDLINE=9829611; PubMed=9630610;   | 93.2  | 91.5        | 316    | 11    | O35545      |
| RA       | Yamaji R., Murakami C., Takenoshita M., Tsuyama S., Inui H.,             | 93.2  | 91.5        | 316    | 11    | O35545      |
| RA       | Miyatake K., Nakano Y.,  | 93.2  | 91.5        | 316    | 11    | O35545      |
| RT       | "The Intron 5-Inserted form of rat erythropoietin receptor is            | 93.2  | 91.5        | 316    | 11    | O35545      |
| RT       | expressed as a membrane-bound form."                                     | 93.2  | 91.5        | 316    | 11    | O35545      |
| RL       | Biochim. Biophys. Acta 1403:169-178(1998).                               | 93.2  | 91.5        | 316    | 11    | O35545      |
| DR       | EMBL: D83509; BAA22373.1; -  | 93.2  | 91.5        | 316    | 11    | O35545      |
| DR       | HGSP: P19235; IEBA.  | 93.2  | 91.5        | 316    | 11    | O35545      |
| DR       | GO: GO:0016020; C:membrane; IEA.   | 93.2  | 91.5        | 316    | 11    | O35545      |
| DR       | GO: GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA. | 93.2  | 91.5        | 316    | 11    | O35545      |
| DR       | GO: GO:0004872; F:receptor activity; IEA.                                | 93.2  | 91.5        | 316    | 11    | O35545      |
| DR       | InterPro: IPR002996; CRIA.   | 93.2  | 91.5        | 316    | 11    | O35545      |
| DR       | InterPro: IPR003961; FN III.   | 93.2  | 91.5        | 316    | 11    | O35545      |
| DR       | InterPro: IPR008957; FN III-like.  | 93.2  | 91.5        | 316    | 11    | O35545      |
| DR       | InterPro: IPR003528; Hematopoietin_L_F1.                                 | 93.2  | 91.5        | 316    | 11    | O35545      |
| DR       | Pfam: PF00041; fn3; 1.   | 93.2  | 91.5        | 316    | 11    | O35545      |
| DR       | SMART: SM00060; FN3; 1.  | 93.2  | 91.5        | 316    | 11    | O35545      |
| DR       | PROSITE: PS01352; HEMATOPOI_REC_L_F1; 1.                                 | 93.2  | 91.5        | 316    | 11    | O35545      |
| KW       | Receptor; signal.  | 93.2  | 91.5        | 316    | 11    | O35545      |
| FT       | SIGNAL   | 93.2  | 91.5        | 316    | 11    | O35545      |
| FT       | CHAIN  | 93.2  | 91.5        | 316    | 11    | O35545      |
| SO       | SEQUENCE   | 93.2  | 91.5        | 316    | 11    | O35545      |

Query Match 93.2%; Score 109; DB 11; Length 316;  
Best Local Similarity 91.3%; Pred. No. 6.8e-10;

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Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 QRVFLLGRTCTVLSNRGRTY 23
Db 193 QRVFLLGRTCTVLSNRGRTY 215

RESULT 2
Q9MYZ9 PRELIMINARY; PRT; 509 AA.
ID Q9MYZ9
AC Q9MYZ9;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Erythropoietin receptor.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Pearson F.L., Smith T.P.L., Sonstegard T.S., Klemcke H.G.,
RA Christenson R.K., Vallet J.L.;
RT "Porcine Erythropoietin Receptor: Molecular Cloning and Expression in
RT Embryonic and Fetal Liver.";
RT Domest. Anim. Endocrinol. 0:0-0(2000).
DR EMBL; AF274305; AA677065.1; -.
DR HSSP; P19235; IERN.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003528; Hemtopoptn_L_Fl.
DR InterPro; IPR000572; Oxidored_mol_yb.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_Fl; 1.
DR PROSITE; PS00559; MOLYDOPTERIN_EUK; 1.
KM Receptor.
SQ SEQUENCE 509 AA; 55183 MW; 35B565D07C6BCDBA CRC64;

Query Match 91.5%; Score 107; DB 6; Length 509;
Best Local Similarity 91.3%; Pred. No. 2.5e-09;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 QRVFLLGRTCTVLSNRGRTY 23
Db 195 QRVFLLGRTCTVLSNRGRTY 217

RESULT 3
Q28206 PRELIMINARY; PRT; 229 AA.
ID Q28206
AC Q28206;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DE 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Erythropoietin receptor (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Sullivan H.B., Feldman B.F., Majiwa P.A.O., Logan-Henfrey L.L.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
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DR EMBL; U61399; AAB03871.1; -.
DR HSSP; P19235; IEBA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003528; Hemtopoptn_L_Fl.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_Fl; 1.
KM Receptor.
FT NON_TER 1 1
FT NON_TER 229 229
SQ SEQUENCE 229 AA; 25170 MW; EDFAA6F110D992E8 CRC64;

Query Match 88.9%; Score 104; DB 6; Length 229;
Best Local Similarity 87.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 QRVFLLGRTCTVLSNRGRTY 23
Db 136 QRVFLLGRTCTVLSNRGRTY 158

RESULT 4
Q27950 PRELIMINARY; PRT; 229 AA.
ID Q27950
AC Q27950;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DE 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Erythropoietin receptor (Fragment).
OS Bos indicus (Zebu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
NCBI_TaxID=9915;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Sullivan H.B., Feldman B.F., Majiwa P.A.O., Logan-Henfrey L.L.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U61398; AAB03870.1; -.
DR HSSP; P19235; IEBA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003528; Hemtopoptn_L_Fl.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_Fl; 1.
KM Receptor.
FT NON_TER 1 1
FT NON_TER 229 229
SQ SEQUENCE 229 AA; 25196 MW; F6E01C4AB07893E8 CRC64;

Query Match 88.9%; Score 104; DB 6; Length 229;
Best Local Similarity 87.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 QRVFLLGRTCTVLSNRGRTY 23
Db 136 QRVFLLGRTCTVLSNRGRTY 158

RESULT 5
Q95N13
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ID Q95N13 PRELIMINARY; PRT; 387 AA.
AC Q95N13;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Erythropoietin receptor (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA David B., Lam G.B., Moritz K.M., Koukoulas I., Wintour M.;
RT "Quantitation of the mRNA levels of Epo and Epor in various tissues in
the ovine fetus."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY029232; AAK3873.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003528; FN_III-like.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
DR Receptor.
KW NON_TER
FT NON_TER 1 387
SQ SEQUENCE 387 AA; 42039 MW; 0D1E6173C432EBC6 CRC64;

Query Match 88.9%; Score 104; DB 6; Length 387;
Best Local Similarity 87.0%; Pred. No. 5.9e-09;
Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QRVETLGRTECVLSNLRGRTRY 23
Db 130 QRVETLGRTECVLSNLRGRTRY 152

RESULT 6
Q95N14 PRELIMINARY; PRT; 418 AA.
AC Q95N14;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Erythropoietin receptor (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA David B., Lam G.B., Moritz K.M., Koukoulas I., Wintour M.;
RT "Quantitation of the mRNA levels of Epo and Epor in various tissues in
the ovine fetus."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY029231; AAK38170.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003528; Hemtopoptn_L_F1.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
DR Receptor.
KW NON_TER
FT NON_TER 1 418
SQ SEQUENCE 418 AA; 45282 MW; BB742EBEA034503C CRC64;
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SQ SEQUENCE 418 AA; 45282 MW; BB742EBEA034503C CRC64;

Query Match 88.9%; Score 104; DB 6; Length 418;
Best Local Similarity 87.0%; Pred. No. 6.4e-09;
Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QRVETLGRTECVLSNLRGRTRY 23
Db 130 QRVETLGRTECVLSNLRGRTRY 152

RESULT 7
Q9U052 PRELIMINARY; PRT; 176 AA.
AC Q9U052;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Uncharacterized protein.
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
OC NCBI_TaxID=2320;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=AV19 / DSM 6324 / JCM 9639;
RX MEDLINE=21927647; PubMed=11930014;
RA Slesarev A.I., Mezheva K.V., Makarova K.S., Polushin N.N.,
RA Shcherbina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natsale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA Malyskh A.G., Koonin E.V., Kozhavkin S.A.;
RT "The complete genome of hyperthermophile methanopyrus kandleri AV19
and monophyly of archaeal methanogens."
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
DR EMBL; AE010332; AM01560.1; -.
DR InterPro; IPR009003; Cys_Ser_trypsin.
KW Complete proteome.
SQ SEQUENCE 176 AA; 19285 MW; 81E181C7BF3BDB08 CRC64;

Query Match 47.9%; Score 56; DB 17; Length 176;
Best Local Similarity 52.4%; Pred. No. 0.3;
Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 2 RVEILGRTECVLSNLRGRTRY 22
Db 150 RMDVIBERTALKRLRGROR 170

RESULT 8
Q9U052 PRELIMINARY; PRT; 1028 AA.
AC Q9U052;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Neural adhesion molecule NB-3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kamei Y., Teutsuni O., Taketani Y., Watanabe K.;
RT "DNA cloning and chromosomal localization of neural adhesion
molecule, NB-3 in human."
RL J. Neurosci. Res. 51:275-283(1998).
DR EMBL; AB003592; BA082612.1; -.
DR HSSP; P20241; ICFB.
DR Genew; HGNC:2176; CNTN6.
DR GO; GO:0007155; P:cell adhesion; TAS.
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DR GO:000717, P:central nervous system development; TAS.
DR InterPro: IPR003439; ABC_transporter.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003598; Ig_c2.
DR Pfam: PF00041; fn3; 4.
DR Pfam: PF00047; Ig; 6.
DR SMART: SM00060; FN3; 3.
DR SMART: SM00408; IGC2; 5.
DR PROSITE: PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE: PS50835; IG_LIKE; 6.
DR Immunoglobulin domain.
SQ SEQUENCE 1028 AA; 113956 MW; 8B5A2BD2F2936A6 CRC64;

Query Match 44.4%; Score 52; DB 4; Length 1028;
Best Local Similarity 71.4%; Pred. No. 9.9;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 EGRTCYLSNLRGR 20
Db 292 EGFYECLASNLNRGR 305

RESULT 9
Q9AKX8 PRELIMINARY; PRT; 826 AA.
AC Q9AKX8;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Legionella pneumophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OC NCBI_TaxID=446;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=serogroup 1;
RX MEDLINE=21150471; PubMed=11251842;
RA Iweneberg E., Mayer B., Deryab N., Kooistra O., Zaehner U.,
Ronde M., Swanson J., Froesch M.;
RT "Chromosomal insertion and excision of a 30 kb insatible genetic
element is responsible for phase variation of lipopolysaccharide and
RT other virulence determinants in Legionella pneumophila.";
RL Mol. Microbiol. 39:1259-1271(2001).
DR EMBL: AJ277755; CAC33467.1; -.
KW Hypothetical protein.
SQ SEQUENCE 826 AA; 91581 MW; 4BD540C2665CFEF CRC64;

Query Match 41.9%; Score 49; DB 2; Length 826;
Best Local Similarity 42.9%; Pred. No. 25;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 QRVLEIGRTCYLSNLRGR 21
Db 782 RRAESNEGRLETTIESLKGRS 802

RESULT 10
P97528 PRELIMINARY; PRT; 1028 AA.
AC P97528;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE NB-3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=Wistar; TISSUE=Brain;
RX MEDLINE=97101230; PubMed=8945756;
RA Ogawa J., Kaneko H., Masuda T., Nagata S., Hosoya H., Watanabe K.;
RT "Novel neural adhesion molecules in the Contactin/F3 subgroup of the
RT immunoglobulin superfamily: Isolation and characterization of cDNAs
RT from rat brain.";
RL Neurosci. Lett. 218:173-176(1996).
DR EMBL: D87248; BA013320.1; -.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0004009; F:ATP-binding cassette (ABC) transporter acti. .; IEA.
DR GO: GO:0006109; P:transport; IEA.
DR InterPro: IPR003439; ABC_transporter.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003598; Ig_c2.
DR Pfam: PF00041; fn3; 4.
DR Pfam: PF00047; Ig; 6.
DR SMART: SM00060; FN3; 4.
DR SMART: SM00408; IGC2; 5.
DR PROSITE: PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE: PS50835; IG_LIKE; 6.
DR Immunoglobulin domain.
SQ SEQUENCE 1028 AA; 114065 MW; 47EPD8A370CF4923 CRC64;

Query Match 41.9%; Score 49; DB 11; Length 1028;
Best Local Similarity 71.4%; Pred. No. 32;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 EGRTCYLSNLRGR 20
Db 292 EGFYECLASNLNRGR 305

RESULT 11
Q9LPY7 PRELIMINARY; PRT; 428 AA.
AC Q9LPY7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE T3J3J18.14.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot; rosids;
OC euroside II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shim P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
RA Kim C., Aliafi H., Bet O., Chin C., Chou J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharbek N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thavert A.,
RA Tortini M., Vayberg M., Yu G., Federspiel N.A., Thellogis A.,
RA Becker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC T3J3J18 from chromosome
RT 1.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC011661; AAF16632.1; -.
SQ SEQUENCE 428 AA; 48982 MW; 603F3FF2725622F9 CRC64;

Query Match 45.5%; Score 48; DB 10; Length 428;
Best Local Similarity 45.5%; Pred. No. 18;
Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 QRVLEIGRTCYLSNLRGR 22
Db 132 KRPQLENTLTLITSTRGR 153

RESULT 12

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O9JMB8
ID O9JMB8 PRELIMINARY; PRT; 1028 AA.
AC O9JMB8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Neural recognition molecule NB-3.
GN CNTN6 OR MNB-3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129SVJ; TISSUE=Brain;
RX MEDLINE=20183687; PubMed=10717476;
RA Lee S., Takeda Y., Kawano H., Hosoya H., Nomoto M., Fujimoto D.,
RA Takahashi N., Watanabe K.;
RT "Expression and regulation of a gene encoding neural recognition
RT molecule NB-3 of the contactin/r3 subgroup in mouse brain.";
RL Gene 245:253-266(2000).
CC -; SIMILARITY: CONTAINS 6 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
DR EMBL; AB032602; BAA92367.1; -.
DR HSSP; P20241; ICFB.
DR MGD; MGI:1858223; Cntn6.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003439; ABC transporter.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR007110; Ig_II-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; fn3; 4.
DR SMART; SM00060; FN3; 4.
DR SMART; SM00408; IGC2; 5.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS50835; IG_LIKE; 6.
DR PROSITE; PS00290; IG_MHC; 1.
KM Immunoglobulin domain.
SQ SEQUENCE 1028 AA; 113759 MW; AEECS9F86CA3978F CRC64;

Query Match 41.0%; Score 48; DB 11; Length 1028;
Best Local Similarity 64.3%; Pred. No. 47;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 7 EGRTECVLSNLGR 20
DB 292 EGFECTAGNLGR 305

RESULT 13
O8C6X1 PRELIMINARY; PRT; 1028 AA.
ID O8C6X1;
AC O8C6X1;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Contactin 6.
GN CNTN6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;

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RT RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK052872; BAC35227.1; -.
DR MGD; MGI:1858223; Cntn6.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003439; ABC transporter.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig_II-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; fn3; 4.
DR Pfam; PF00047; fn3; 4.
DR SMART; SM00060; FN3; 4.
DR SMART; SM00409; IG; 6.
DR SMART; SM00408; IGC2; 6.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS50835; IG_LIKE; 6.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 1028 AA; 113761 MW; B23ED3008B1B101 CRC64;

Query Match 41.0%; Score 48; DB 11; Length 1028;
Best Local Similarity 64.3%; Pred. No. 47;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 7 EGRTECVLSNLGR 20
DB 292 EGFECTAGNLGR 305

RESULT 14
O94LS6 PRELIMINARY; PRT; 539 AA.
ID O94LS6;
AC O94LS6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxId=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Beil C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,
RA Brenner M., Burgess S., Hance M., Shvartsbeyn M., Teltzin T.,
RA Riggs F., Heiao J., Zisemann V., Blunt S., Pal G., Vanaken S.E.,
RA Utecherback T.R., Feldblyum T.V., Quackenbush J., Salberg S.L.,
RA White O., Fraser C.M.;
RT "Oryza sativa chromosome 10 BAC OSJNB0011A08 genomic sequence.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC034258; AAK54287.1; -.
DR Gramene; O94LS6; -.
KM Hypothetical protein.
SQ SEQUENCE 539 AA; 60201 MW; 8EBED40239310BC2 CRC64;

Query Match 40.2%; Score 47; DB 10; Length 539;
Best Local Similarity 56.2%; Pred. No. 34;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 4 EILEGTECVLSNLGR 19
DB 9 EVHGBTRSCVLLNVRG 24

RESULT 15

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07XDN4
ID 07XDN4 PRELIMINARY; PRT; 539 AA.
AC 07XDN4;
DT 01-OCT-2003 (TReMBrel. 25, Created)
DT 01-OCT-2003 (TReMBrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBrel. 25, Last annotation update)
DE Hypoetical protein.
GN OSJNB0011A08.11.
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_taxid=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA The Rice Chromosome 10 Sequencing Consortium;
RT "in-depth view of structure, activity, and evolution of rice
   chromosome 10.";
RL Science 300:1566-1569(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017102; AAP54107.1; -.
KM Hypoetical protein.
SQ SEQUENCE 539 AA; 60201 MW; 8EBED40239310BC2 CRC64;

Query Match 40.2%; Score 47; DB 10; Length 539;
Best Local Similarity 56.2%; Pred. No. 34;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 4 EILGRTCTVLSNLRG 19
   | : ||| | : ||
Db 9 EVHGGTRSCVLTNVRG 24

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Search completed: May 6, 2004, 12:46:18  
 Job time : 40 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: May 6, 2004, 12:40:41, Search time 11 Seconds  
(without alignments)  
108.874 Million cell updates/sec

Title: US-10-612-885A-1  
Perfect score: 117

Sequence: 1 QRVLEIGRECTLSNLRGRTRY 23

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 117   | 100.0       | 508    | 1  | EPOR_HUMAN  |
| 2          | 109   | 93.2        | 507    | 1  | EPOR_MOUSE  |
| 3          | 109   | 93.2        | 507    | 1  | EPOR_RAT    |
| 4          | 49    | 41.9        | 221    | 1  | GIDB_BIFLO  |
| 5          | 49    | 41.9        | 473    | 1  | KRM1_MOUSE  |
| 6          | 49    | 41.9        | 475    | 1  | KRM1_HUMAN  |
| 7          | 48    | 41.0        | 312    | 1  | PYRB_COREF  |
| 8          | 48    | 41.0        | 312    | 1  | PYRB_COREG  |
| 9          | 47    | 40.2        | 956    | 1  | TSP3_HUMAN  |
| 10         | 46    | 39.3        | 58     | 1  | YSS9_ENTFA  |
| 11         | 46    | 39.3        | 67     | 1  | RS28_KL0LA  |
| 12         | 46    | 39.3        | 67     | 1  | RS28_KL0LA  |
| 13         | 46    | 39.3        | 489    | 1  | C128_MYCTU  |
| 14         | 46    | 39.3        | 697    | 1  | AMS2_SCHPO  |
| 15         | 46    | 39.3        | 1609   | 1  | YLS4_CAREL  |
| 16         | 45.5  | 38.9        | 607    | 1  | DB10_NICSY  |
| 17         | 45    | 38.5        | 512    | 1  | YR33_MYCTU  |
| 18         | 45    | 38.5        | 1036   | 1  | AXOI_CHICK  |
| 19         | 44    | 37.6        | 473    | 1  | KRM1_RAT    |
| 20         | 43.5  | 37.2        | 269    | 1  | PPG_VIBPA   |
| 21         | 43    | 36.8        | 486    | 1  | MURC_COREG  |
| 22         | 43    | 36.8        | 956    | 1  | TSP3_MOUSE  |
| 23         | 42.5  | 36.3        | 228    | 1  | YAZ9_TREPA  |
| 24         | 42.5  | 36.3        | 1912   | 1  | PTPD_HUMAN  |
| 25         | 42    | 35.9        | 667    | 1  | SHAS_YEAST  |
| 26         | 42    | 35.9        | 365    | 1  | DHAS_YEAST  |
| 27         | 42    | 35.9        | 482    | 1  | THII_SALTI  |
| 28         | 42    | 35.9        | 482    | 1  | THII_SALTI  |
| 29         | 42    | 35.9        | 661    | 1  | HCTC_PANIN  |
| 30         | 42    | 35.9        | 1020   | 1  | CONT_MOUSE  |
| 31         | 42    | 35.9        | 1021   | 1  | CONT_MOUSE  |
| 32         | 41.5  | 35.5        | 1897   | 1  | PTPF_HUMAN  |
| 33         | 41    | 35.0        | 94     | 1  | VE7_HPV37   |

## ALIGNMENTS

| RESULT 1 | EPOR_HUMAN   | STANDARD; | PRT; | 508 AA. |
|----------|--|-----------|------|---------|
| AC       | P19235;  |           |      |         |
| DT       | 01-NOV-1990 (Rel. 16, Created)                                       |           |      |         |
| DT       | 15-MAR-2004 (Rel. 43, Last sequence update)                          |           |      |         |
| DE       | Erythropoietin receptor precursor (EPO-R).                           |           |      |         |
| GN       | EPOR.  |           |      |         |
| OS       | Homo sapiens (Human).  |           |      |         |
| OC       | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;              |           |      |         |
| OC       | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.            |           |      |         |
| OX       | NCBI_Taxid=9606;   |           |      |         |
| RN       | [1]  |           |      |         |
| RP       | SEQUENCE FROM N.A.   |           |      |         |
| RX       | MEDLINE=9137359; PubMed=1654273;                                     |           |      |         |
| RA       | Etremman K., St John T.;   |           |      |         |
| RT       | "The erythropoietin receptor gene: cloning and identification of     |           |      |         |
| RT       | multiple transcripts in an erythroid cell line OCIM1."               |           |      |         |
| RL       | Exp. Hematol. 19:973-977(1991).                                      |           |      |         |
| RN       | [2]  |           |      |         |
| RP       | SEQUENCE FROM N.A.   |           |      |         |
| RX       | MEDLINE=90304340; PubMed=2163696;                                    |           |      |         |
| RA       | Jones S.S., D'Andrea A.D., Haines L.L., Wong G.G.;                   |           |      |         |
| RT       | "Human erythropoietin receptor: cloning, expression, and biologic    |           |      |         |
| RT       | characterization."   |           |      |         |
| RL       | Blood 76:31-35(1990).  |           |      |         |
| RN       | [3]  |           |      |         |
| RP       | SEQUENCE FROM N.A.   |           |      |         |
| RC       | TISSUE=Placenta;   |           |      |         |
| RX       | MEDLINE=92399733; PubMed=1668606;                                    |           |      |         |
| RA       | Noguchi C.T., Bae K.S., Chin K., Wada Y., Schechter A.N.,            |           |      |         |
| RT       | Hankins W.D.;  |           |      |         |
| RT       | "Cloning of the human erythropoietin receptor gene."                 |           |      |         |
| RL       | Blood 78:2548-2556(1991).  |           |      |         |
| RN       | [4]  |           |      |         |
| RP       | SEQUENCE OF 1-96 FROM N.A.   |           |      |         |
| RC       | TISSUE=Placenta;   |           |      |         |
| RX       | MEDLINE=92399734; PubMed=1668607;                                    |           |      |         |
| RA       | Mouche U., Tournamille C., Hattab C., Boffa G., Carttron J.-P.,      |           |      |         |
| RT       | Chretien S.;   |           |      |         |
| RT       | "Cloning of the gene encoding the human erythropoietin receptor."    |           |      |         |
| RL       | Blood 78:2557-2563(1991).  |           |      |         |
| RN       | [5]  |           |      |         |
| RP       | SEQUENCE OF 1-17 FROM N.A.   |           |      |         |
| RX       | MEDLINE=92147143; PubMed=1664413;                                    |           |      |         |
| RA       | Penny L.A., Forget B.G.;   |           |      |         |
| RT       | "Genomic organization of the human erythropoietin receptor gene."    |           |      |         |
| RL       | Genomics 11:974-980(1991).   |           |      |         |
| RN       | [6]  |           |      |         |
| RP       | PHOSPHORYLATION AND INTERACTION WITH APS.                            |           |      |         |
| RX       | MEDLINE=9301417; PubMed=10374881;                                    |           |      |         |
| RA       | Wakita T., Sasaki A., Mitsui K., Yokouchi M., Inoue A., Komiya S.,   |           |      |         |
| RA       | Yoshimura A.;  |           |      |         |
| RT       | "APS, an adaptor protein containing Pleckstrin homology (PH) and Src |           |      |         |
| RT       | homology-2 (SH2) domains inhibits the JAK-STAT pathway in            |           |      |         |

Q97b95 thermoplasma  
P77161 escherichia  
O60041 thermotoga  
O9a2x6 caudobacter  
O29265 archaeoglob  
P38867 saccharomyc  
P23760 homo sapien  
P24610 mus musculu  
P23759 homo sapien  
P1141 caenorhabdi  
O52225 thermus fil  
P32670 escherichia





RN [1] SEQUENCE FROM N.A.  
 RX MEDLINE=69195238; PubMed=2539263;  
 RA D'Andrea A.D., Lodish H.F., Wong G.G.;  
 RT "Expression cloning of the murine erythropoietin receptor.";  
 RL Cell 57:277-285(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c; TISSUE=Liver;  
 RX MEDLINE=91080149; PubMed=2175360;  
 RA Kuramochi S., Ikawa Y., Todokoro K.;  
 RT "Characterization of murine erythropoietin receptor genes.";  
 RL J. Mol. Biol. 216:567-575(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92017832; PubMed=1656233;  
 RA Hino M., Tojo A., Misawa Y., Morii H., Takaku F., Shibuya M.;  
 RT "Unregulated expression of the erythropoietin receptor gene caused by  
 RT insertion of spleen focus-forming virus long terminal repeat in a  
 RT murine erythroleukemia cell line.";  
 RL Mol. Cell. Biol. 11:5527-5533(1991).  
 RN [4]  
 RP SEQUENCE OF 1-27 FROM N.A.  
 RX MEDLINE=99287158; PubMed=2162479;  
 RA Youssoufian H., Zon L.I., Orkin S.H., D'Andrea A.D., Lodish H.F.;  
 RT "Structure and transcription of the mouse erythropoietin receptor  
 RT gene.";  
 RL Mol. Cell. Biol. 10:3675-3682(1990).  
 RN [5]  
 RP SEQUENCE OF 1-24 FROM N.A.  
 RX MEDLINE=91201346; PubMed=1849897;  
 RA Lacombe C., Chretien S., Lemarchandel V., Mayeux P., Romeo P.H.,  
 RA Gieselbrecht S., Carton J.-P.;  
 RT "Spleen focus-forming virus long terminal repeat insertion  
 RT activation of the murine erythropoietin receptor gene in the T3C1-2  
 RT friend leukemia cell line.";  
 RL J. Biol. Chem. 266:6952-6956(1991).  
 RN [6]  
 RP INTERACTION WITH APS.  
 RX MEDLINE=22510236; PubMed=1244928;  
 RA Wolberg P., Lemarsson J., Gottfridsson E., Yoshimura A.,  
 RA Romstrand L.;  
 RT "The adapter protein APS associates with the multifunctional docking  
 RT sites Tyr-568 and Tyr-936 in c-Klt.";  
 RL Biochem. J. 370:1033-1038(2003).  
 RN [7]  
 RP MUTAGENESIS.  
 RX MEDLINE=93180826; PubMed=8382775;  
 RA Miura O., Cleveland J.L., Ihle J.N.;  
 RT "Inactivation of erythropoietin receptor function by point mutations  
 RT in a region having homology with other cytokine receptors.";  
 RL Mol. Cell. Biol. 13:1788-1795(1993).  
 CC -1- FUNCTION: Receptor for erythropoietin. Mediates erythropoietin-  
 CC induced erythroblasts proliferation and differentiation. Upon EPO  
 CC stimulation, EPOR dimerizes triggering the JAK2/STAT5 signaling  
 CC cascade. Isoform 2 acts as a dominant-negative receptor for EPOR-  
 CC mediated signals.  
 CC -1- SUBUNIT: Interacts with APS.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors.  
 CC Subfamily 1.  
 CC -1- SIMILARITY: Contains 1 fibronectin type III domain.  
 CC -----  
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 CC -----  
 CC EMBL; J04843; AAA37571.1; -.  
 DR EMBL; X53081; CAA37248.1; -.

| Query                 | 1                        | ORVELLEGRECTCVLSNLGRTRY                | 23                                 |
|-----------------------|--------------------------|--|------------------------------------|
| Db                    | 193                      | QREVELERTECVLSNLGGTRY                  | 215                                |
| Query Match           |                          | 93.2%;                                 | Score 109; DB 1; Length 507;       |
| Best Local Similarity |                          | 91.3%;                                 | Pred. No. 1.5e-09;                 |
| Matches               | 21;                      | Conservative                           | 1; Mismatches 1; Indels 0; Gaps 0; |
| Dr                    | EMBL; M38133;            | AAA37572.1;                            | -                                  |
| Dr                    | EMBL; M62360;            | AAA37582.1;                            | -                                  |
| Dr                    | EMBL; S59388;            | AAB20029.2;                            | -                                  |
| Dr                    | PIR; A41686;             | A43385.                                |                                    |
| Dr                    | PIR; S14081;             | S14081.                                |                                    |
| Dr                    | HSSP; P19235;            | IEBA.                                  |                                    |
| Dr                    | MED; MGI:95408;          | Epor.                                  |                                    |
| Dr                    | InterPro; IPR002996;     | CRIA.                                  |                                    |
| Dr                    | InterPro; IPR008957;     | FN_III-11ke.                           |                                    |
| Dr                    | InterPro; IPR003961;     | FN_III.                                |                                    |
| Dr                    | InterPro; IPR00328;      | Hemtopopn_L_F1.                        |                                    |
| Dr                    | Pfam; PF00041;           | fn3. 1.                                |                                    |
| Dr                    | PIRSF; PIRSF01959;       | Epo_receptor. 1.                       |                                    |
| Dr                    | SMART; SM0060;           | FN3. 1.                                |                                    |
| Dr                    | PROSITE; PS01352;        | HEMATOPO_REC_L_F1. 1.                  |                                    |
| KV                    | Receptor; Transmembrane; | Glycoprotein; Signal; Phosphorylation. |                                    |
| FT                    | SIGNAL                   | 1                                      | 24                                 |
| FT                    | CHAIN                    | 25                                     | 507                                |
| FT                    | DOMAIN                   | 25                                     | 249                                |
| FT                    | TRANSMEM                 | 250                                    | 272                                |
| FT                    | DOMAIN                   | 273                                    | 507                                |
| FT                    | DOMAIN                   | 147                                    | 212                                |
| FT                    | SITE                     | 367                                    | 367                                |
| FT                    | DISULFID                 | 52                                     | 62                                 |
| FT                    | DISULFID                 | 90                                     | 106                                |
| FT                    | MOD_RES                  | 367                                    | 367                                |
| FT                    | CARBOHYD                 | 75                                     | 75                                 |
| FT                    | CONFLICT                 | 291                                    | 291                                |
| FT                    | SEQUENCE                 | 507 AA;                                | 55194 MW; 067657A2E26451CA CRC64;  |
| Dr                    | EMBL; M38133;            | AAA37572.1;                            | -                                  |
| Dr                    | EMBL; M62360;            | AAA37582.1;                            | -                                  |
| Dr                    | EMBL; S59388;            | AAB20029.2;                            | -                                  |
| Dr                    | PIR; A41686;             | A43385.                                |                                    |
| Dr                    | PIR; S14081;             | S14081.                                |                                    |
| Dr                    | HSSP; P19235;            | IEBA.                                  |                                    |
| Dr                    | MED; MGI:95408;          | Epor.                                  |                                    |
| Dr                    | InterPro; IPR002996;     | CRIA.                                  |                                    |
| Dr                    | InterPro; IPR008957;     | FN_III-11ke.                           |                                    |
| Dr                    | InterPro; IPR003961;     | FN_III.                                |                                    |
| Dr                    | InterPro; IPR00328;      | Hemtopopn_L_F1.                        |                                    |
| Dr                    | Pfam; PF00041;           | fn3. 1.                                |                                    |
| Dr                    | PIRSF; PIRSF01959;       | Epo_receptor. 1.                       |                                    |
| Dr                    | SMART; SM0060;           | FN3. 1.                                |                                    |
| Dr                    | PROSITE; PS01352;        | HEMATOPO_REC_L_F1. 1.                  |                                    |
| KV                    | Receptor; Transmembrane; | Glycoprotein; Signal; Phosphorylation. |                                    |
| FT                    | SIGNAL                   | 1                                      | 24                                 |
| FT                    | CHAIN                    | 25                                     | 507                                |
| FT                    | DOMAIN                   | 25                                     | 249                                |
| FT                    | TRANSMEM                 | 250                                    | 272                                |
| FT                    | DOMAIN                   | 273                                    | 507                                |
| FT                    | DOMAIN                   | 147                                    | 212                                |
| FT                    | SITE                     | 367                                    | 367                                |
| FT                    | DISULFID                 | 52                                     | 62                                 |
| FT                    | DISULFID                 | 90                                     | 106                                |
| FT                    | MOD_RES                  | 367                                    | 367                                |
| FT                    | CARBOHYD                 | 75                                     | 75                                 |
| FT                    | CONFLICT                 | 291                                    | 291                                |
| FT                    | SEQUENCE                 | 507 AA;                                | 55194 MW; 067657A2E26451CA CRC64;  |
| Dr                    | EMBL; M38133;            | AAA37572.1;                            | -                                  |
| Dr                    | EMBL; M62360;            | AAA37582.1;                            | -                                  |
| Dr                    | EMBL; S59388;            | AAB20029.2;                            | -                                  |
| Dr                    | PIR; A41686;             | A43385.                                |                                    |
| Dr                    | PIR; S14081;             | S14081.                                |                                    |
| Dr                    | HSSP; P19235;            | IEBA.                                  |                                    |
| Dr                    | MED; MGI:95408;          | Epor.                                  |                                    |
| Dr                    | InterPro; IPR002996;     | CRIA.                                  |                                    |
| Dr                    | InterPro; IPR008957;     | FN_III-11ke.                           |                                    |
| Dr                    | InterPro; IPR003961;     | FN_III.                                |                                    |
| Dr                    | InterPro; IPR00328;      | Hemtopopn_L_F1.                        |                                    |
| Dr                    | Pfam; PF00041;           | fn3. 1.                                |                                    |
| Dr                    | PIRSF; PIRSF01959;       | Epo_receptor. 1.                       |                                    |
| Dr                    | SMART; SM0060;           | FN3. 1.                                |                                    |
| Dr                    | PROSITE; PS01352;        | HEMATOPO_REC_L_F1. 1.                  |                                    |
| KV                    | Receptor; Transmembrane; | Glycoprotein; Signal; Phosphorylation. |                                    |
| FT                    | SIGNAL                   | 1                                      | 24                                 |
| FT                    | CHAIN                    | 25                                     | 507                                |
| FT                    | DOMAIN                   | 25                                     | 249                                |
| FT                    | TRANSMEM                 | 250                                    | 272                                |
| FT                    | DOMAIN                   | 273                                    | 507                                |
| FT                    | DOMAIN                   | 147                                    | 212                                |
| FT                    | SITE                     | 367                                    | 367                                |
| FT                    | DISULFID                 | 52                                     | 62                                 |
| FT                    | DISULFID                 | 90                                     | 106                                |
| FT                    | MOD_RES                  | 367                                    | 367                                |
| FT                    | CARBOHYD                 | 75                                     | 75                                 |
| FT                    | CONFLICT                 | 291                                    | 291                                |
| FT                    | SEQUENCE                 | 507 AA;                                | 55194 MW; 067657A2E26451CA CRC64;  |
| Dr                    | EMBL; M38133;            | AAA37572.1;                            | -                                  |
| Dr                    | EMBL; M62360;            | AAA37582.1;                            | -                                  |
| Dr                    | EMBL; S59388;            | AAB20029.2;                            | -                                  |
| Dr                    | PIR; A41686;             | A43385.                                |                                    |
| Dr                    | PIR; S14081;             | S14081.                                |                                    |
| Dr                    | HSSP; P19235;            | IEBA.                                  |                                    |
| Dr                    | MED; MGI:95408;          | Epor.                                  |                                    |
| Dr                    | InterPro; IPR002996;     | CRIA.                                  |                                    |
| Dr                    | InterPro; IPR008957;     | FN_III-11ke.                           |                                    |
| Dr                    | InterPro; IPR003961;     | FN_III.                                |                                    |
| Dr                    | InterPro; IPR00328;      | Hemtopopn_L_F1.                        |                                    |
| Dr                    | Pfam; PF00               |  |                                    |

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CC -----

DR EMBL, D13566; BAA02761.1; -.  
 DR PIR, A46713; A46713.  
 DR HSSP, P19235; IEBA.  
 DR InterPro: IPRO02996; CRA.  
 DR InterPro: IPRO08957; FN\_III-like.  
 DR InterPro: IPRO03961; FN\_III.  
 DR InterPro: IPRO03528; Hemioptn\_L\_Fl.  
 DR Pfam; PF00041; fn3; 1.  
 DR PIRSF; PIRSF01959; EPO\_receptor; 1.  
 DR SMART; SM00060; FN3; 1.  
 DR PROSITE; PS01352; HEMATOPO\_REC\_L\_Fl; 1.  
 DR Receptor; Transmembrane; Glycoprotein; Signal.  
 KM SIGNAL 1  
 FT CHAIN 1 24  
 FT CHAIN 25 507  
 FT DOMAIN 25 249 ERYTHROPOIETIN RECEPTOR.  
 FT TRANSMEM 250 272 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 273 507 POTENTIAL.  
 FT DOMAIN 147 212 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 52 62 FIBRONECTIN TYPE-III.  
 FT DISULFID 90 106 BY SIMILARITY.  
 FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 507 AA; 55499 MW; AC79AF22D06A7312 CRC64;

Query Match 93.2%; Score 109; DB 1; Length 507;  
 Best Local Similarity 91.3%; Pred. No. 1.5e-09;  
 Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QVVELEGRTCVSNLRGRTRY 23  
 Db 193 QVVELEGRTCVSNLRGRTRY 215

RESULT 4  
 GIDB\_BIFLO STANDARD; PRT; 221 AA.  
 AC Q86604;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Methyltransferase gids (EC 2.1.1.-) (Glucose inhibited division  
 DE protein B).  
 GN GIDB OR BL0646.  
 OS Bifidobacterium longum.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;  
 CC Bifidobacteriaceae; Bifidobacterium.  
 OX NCBI\_TaxID=216816;  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NCC 2705;  
 RX MEDLINE=22294977; PubMed=12381787;  
 RA Schell M.A., Karimantzou M., Snel B., Vilanova D., Berger B.,  
 RA Peesi G., Zwaahlen M.-C., Desiere F., Bork P., Delley M.,  
 RA Fridmore R.D., Arigoni F.  
 RT "The genome sequence of Bifidobacterium longum reflects its adaptation  
 RT to the human gastrointestinal tract."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).  
 CC -1- FUNCTION: Probable S-adenosyl-L-methionine dependent  
 CC methyltransferase specific for a sterol and/or lipid substrate (By  
 CC similarity).  
 CC -1- SIMILARITY: Belongs to the gids family.

CC -----

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CC -----

DR EMBL; AE014686; AAN24468.1; -.  
 DR HAMAP; MF 00074; -; 1.  
 DR InterPro: IPRO03682; Gids.  
 DR Pfam; PF02527; Gids; 1.  
 DR ProDom; PD004441; Gids; 1.  
 DR TIGRFAMs; TIGR00138; gids; 1.  
 DR Transferase; Methyltransferase; Complete proteome.  
 SQ SEQUENCE 221 AA; 24163 MW; FB131A516368A05 CRC64;

Query Match 41.9%; Score 49; DB 1; Length 221;  
 Best Local Similarity 45.0%; Pred. No. 1.8;  
 Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 QVVELEGRTCVSNLRGR 20  
 Db 120 QVVELEGRTCVSNLRGR 139

RESULT 5  
 KRM1\_MOUSE  
 ID KRM1\_MOUSE STANDARD; PRT; 473 AA.  
 AC Q29N43;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Kremen protein 1 precursor (Kringles-containing protein marking the eye  
 DE and the nose) (Dickkopf receptor).  
 GN KREMENT OR KREMEN.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A., DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY.  
 RC TISSUE=Brain, and Kidney;  
 RX MEDLINE=21167372; PubMed=11267660;  
 RA Nakamura T., Aoki S., Kitajima K., Takahashi T., Matsumoto K.,  
 RA Nakamura T.;  
 RT "Molecular cloning and characterization of Kremen, a novel  
 RT kringles-containing transmembrane protein."  
 RL Biochim. Biophys. Acta 1518:63-72(2001).  
 CC -1- FUNCTION: Receptor for Dickkopf protein. Cooperates with Dickkopf  
 CC to block Wnt/beta-catenin signaling (by similarity).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
 CC -1- TISSUE SPECIFICITY: In the adult, widely expressed with high  
 CC levels in heart, lung, kidney, skeletal muscle and testis.  
 CC -1- DEVELOPMENTAL STAGE: In the embryo, expression is first detected  
 CC on day 9 and increases up to day 18. Lower levels are found in  
 CC adult. At 9.5 dpc, expression is localised to the apical  
 CC ectodermal ridge (AER) of the developing fore- and hindlimb buds,  
 CC the telencephalon and the first brachial arch. At 10.5 dpc,  
 CC expression is also observed in the myotome and in sensory tissues  
 CC such as the nasal pit and optic vesicle.  
 CC -1- SIMILARITY: Contains 1 CUB domain.  
 CC -1- SIMILARITY: Contains 1 kringles domain.  
 CC -1- SIMILARITY: Contains 1 WSC domain.

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CC -----

DR EMBL; AB059617; BAB40968.1; -.  
 DR HSSP; P00747; ICEA.  
 DR MGD; MGI:193398; Kremen.  
 DR GO; GO:0016021; C:integral to membrane; NMS.  
 DR InterPro: IPRO00859; CUB.  
 DR InterPro: IPRO00001; Kringles.

|    |  |
|----|--|
| DR | InterPro; IPRO02889; WSC.  |
| DR | Pfam; PF00431; CUB; 1.   |
| DR | Pfam; PF00051; kringle1; 1.  |
| DR | Pfam; PF01822; WSC; 1.   |
| DR | PRINTS; PR00018; KRINGLE.  |
| DR | ProDom; PD000395; Kringle; 1.  |
| DR | SMART; SM00042; CUB; 1.  |
| DR | SMART; SM00130; KR; 1.   |
| DR | PROSITE; PS00160; CUB; 1.  |
| DR | PROSITE; PS00021; KRINGLE_1; 1.                                      |
| DR | PROSITE; PS50070; KRINGLE_2; 1.                                      |
| KW | Mut signaling pathway; Signal; Transmembrane; Kringle.<br>POTENTIAL. |
| FT | SIGNAL<br>1 19   |
| FT | CHAIN<br>20 473  |
| FT | DOMAIN<br>21 392   |
| FT | TRANSMEM<br>393 413  |
| FT | DOMAIN<br>414 473  |
| FT | DOMAIN<br>31 114   |
| FT | DOMAIN<br>120 210  |
| FT | DOMAIN<br>214 321  |
| FT | CARBOHYD<br>59 59  |
| FT | CARBOHYD<br>217 217  |
| FT | CARBOHYD<br>255 255  |
| FT | CARBOHYD<br>293 293  |
| FT | CARBOHYD<br>333 333  |
| FT | CARBOHYD<br>345 345  |
| QO | SEQUENCE<br>473 AA; 51716 MW; 58682778BB3FDD1 CR64;                  |

|                       |                |               |          |            |
|-----------------------|----------------|---------------|----------|------------|
| Query Match           | 41.9%          | Score 49      | DB 1     | Length 473 |
| Best Local Similarity | 55.0%          | Pred. No. 4.1 |          |            |
| Matches 11            | Conservative 3 | Mismatches 6  | Indels 0 | Gaps 0     |

```
QY      3 VELEGRTECVLSNLRGTR 22
      ||::|| || ||::|
Db     268 VELDGYTHRVLVRLSGRSR 287
```

## RESULT

| ID | KRM1_HUMAN                      | STANDARD; | PRT; | 475 AA |
|----|---------------------------------|-----------|------|--------|
| AC | Q96MU8; Q9BY70; Q9UGS5; Q9UGU1; |           |      |        |

|    |             |                                   |
|----|-------------|-----------------------------------|
| DT | 28-FEB-2003 | (Rel. 41, Last sequence update)   |
| DT | 10-OCT-2003 | (Rel. 42, Last annotation update) |

DE and the nose) (Dickkopf receptor).

05 Homo sapiens (Human) .  
0C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OX      NCBI_TaxID=9606;
RN      [1]

```

RA Nakamura T., Nakamura T.?  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RI Submitted (OCT-2001) to the EMBL/GenBank/DBI databases

RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 2).

RA Fukuzumi Y., Komiyama M., Sugiyama T., Irie R.,  
RA Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,  
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.

RA  
Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagaatsuma M.  
Murakawa K., Kanehori K., Takahashi-Furii A., Oshima A., Suetivama A.  
RA  
Nawa-Tsuji, Saito K., Nishikawa I., Amano N., Iatsumida H.

RA Kawakami B., Suzuki Y., Sugano S., Nagahara K., Masuno Y., Nagai K.,  
RA Isogai T.;  
PM HUNDO bunseki shugi kenkyukai "chugoku chugyo kyokai" (Japan Association  
of Chugyo)

Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases  
[3]

RX MEDLINE=20057165; PubMed=10591208;  
RA Dunham I., Hunt A.R., Collins J.E.,  
Bruskiewich R., Beare D.M.

RA  
Baguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,  
Clamp M., Smith D.O., Ambrogi R., Almerica J.F., Badger A.N.

RA Buttd C.P., Blakey S.E., Bridgeman A.M., Buck D.P., Burgess J.,  
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,  
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,  
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,  
RA Dhami P.D., Doctrele C., Dodsworth S.J., Durbin R.M., Ellington A.G.,  
RA Evans K.L., Fey J.W., Fleming K., French L., Garner A.A.,  
RA Gilbert J.G.R., Goward M.E., Graham D.V., Griffiths M.N.D., Hall C.,  
RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,  
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,  
RA Laird G.K., Langford C.F., Levesha M.A., Lloyd C., Lloyd D.M.,  
RA Soderlund C., Sproson L., Stewart C.A., Sulston J.E., Swan R.M.,  
RA Vaidin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,  
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,  
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,  
RA Minoshima S., Kasaoki K., Sasaki T., Asakawa S., Kudoh J.,  
RA Shintani A., Shibuya K., Yoshitake Y., Aoki N., Mitsuyma S.,  
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,  
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,  
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,  
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,  
RA Wang Q., Wang Y., Wang Z., White Z., Willingham D., Wu H., Yao Z.,  
RA Zhan M., Zhang G., Chisoso S., Murray J., Miller N., Mink P.,  
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,  
RA Cordes M., Du Z., Fulton L., Goeila D., Graves T., Hawkins J.,  
RA Hinds K., Kemp K., Latreille P., Layman D., Ozeraky P., Rohlfing T.,  
RA Schreier P., Walker C., Wamsley A., Wohlmann P., Pepin K., Nelson J.,  
RA Koef I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,  
RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Salta S.,  
RA Budarf M.L., Mcemerd H.E., Johnson A., Wong A.C.C., Morrow B.E.,  
RA Edelman L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,  
RA Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,  
RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,  
RA Khan A.S., Lane L., Tlathun Y., Wright H.,  
RA "The DNA sequence of human chromosome 22";  
RL Nature 402:489-495(1999).  
CC -I- FUNCTION: Receptor for Dickkopf protein. Cooperates with Dickkopf  
CC to block Wnt/beta-catenin signaling (By similarity).  
CC -I- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -I- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=Q96MU8-1; Sequence=displayed;  
CC Name=2;  
CC IsoId=Q96MU8-2; Sequence=VSP\_003900;  
CC Note=No experimental confirmation available;  
CC -I- SIMILARITY: Contains 1 CUB domain.  
CC -I- SIMILARITY: Contains 1 kringle domain.  
CC -I- SIMILARITY: Contains 1 WSC domain.  
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CC -----  
CC EMBL: AB059618; BAB40969.1; -  
CC EMBL: AK056425; BAB7180.1; -  
CC EMBL: Z95116; CAB62952.1; -  
CC EMBL: AL021393; CAB62959.1; -  
CC Genew; HGNC:17550; KREMN1.  
CC GO: GO:0016021; C:integral to membrane; ISS.  
CC GO: GO:0005624; C:membrane fraction; TAS.  
CC GO: GO:0007154; P:cell communication; TAS.  
CC InterPro: IPR000859; CUB.  
CC InterPro: IPR000001; Kringle.  
CC InterPro: IPR002889; WSC.

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DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00051; Kringles; 1.
DR Pfam; PF01822; WSC; 1.
DR PRINTS; PR00018; KRINGLE.
DR PRODOM; PD000395; Kringles; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS50070; KRINGLE_2; 1.
DR Wnt signaling pathway; Signal; Transmembrane; Kringles;
KW Alternative splicing.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 475 KREMLIN PROTEIN 1.
FT DOMAIN 21 394 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 395 415 POTENTIAL.
FT DOMAIN 416 475 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 33 116 KRINGLE.
FT DOMAIN 121 202 WSC.
FT DOMAIN 216 323 CUB.
FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 219 219 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 347 347 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPIC 473 475 VSD -> A1QDSVTSLSMGQGPRL (in isoform
2).
FT /FTID=VSP_003900.
FT MISSING (IN REF. 1).
FT CONFLICT 29 30 I -> V (IN REF. 2).
FT CONFLICT 206 206 B7E86FDB0F96A04A CRC64;
SQ SEQUENCE 475 AA; 5198 MM; B7E86FDB0F96A04A CRC64;

Query Match 41.9%; Score 49; DB 1; Length 475;
Best Local Similarity 50.0%; Pred. No. 4.1;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 3 VELEGRETCVLSNLRGRT 22
Db 270 VELLGDTTHVLAFFHGRSR 289

RESULT 7
PYR COREF STANDARD; PRT; 312 AA.
AC Q8FTJ9;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate
transcarbamylase) (ATCase).
GN PYR OR C61732.
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=152794;
RX [1]
SEQUENCE FROM N.A.
RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RX MEDLINE=22723752; PubMed=12840036;
RA Nishio Y., Nakamura Y., Kawarabayashi Y., Usuda Y., Kimura E.,
RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
RA Gojobori T.;
RT "Comparative complete genome sequence analysis of the amino acid
RT replacements responsible for the thermostability of Corynebacterium
RT efficiens."
RL Genome Res. 13:1572-1579(2003).
CC -1- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspartate = phosphate
CC + N-carbamoyl-L-aspartate.
CC -1- PATHWAY: Pyrimidine biosynthesis; second step.
CC -1- SIMILARITY: Belongs to the ATCase/OTCase family.
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```
DR EMBL; AP005219; BAB99005.1; -.
DR HAMAP; MF_00001; -; 1.
DR InterPro; IPR006130; Asp/Om Cofact.
DR InterPro; IPR002082; Asp cardmltransf.
DR InterPro; IPR006131; OTCase_O.
DR InterPro; IPR006132; OTCase_P.
DR Pfam; PF00185; OTCase; 1.
DR Pfam; PF02729; OTCase; N; 1.
DR PRINTS; PR00100; AOTCASE.
DR TIGRPFAM; TIGR00670; asp_cab tr; 1.
DR PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
DR Pyrimidine biosynthesis; Transferrase; Complete proteome.
KW SEQUENCE 312 AA; 33706 MM; EEF40AAD98413D3B CRC64;

Query Match 41.0%; Score 48; DB 1; Length 312;
Best Local Similarity 61.1%; Pred. No. 3.7;
Matches 11; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 4 EILEGRETCVLSNLRGRT 21
Db 27 EVLEGRHVKKLPRLRGRT 44

RESULT 8
PYR CORGL STANDARD; PRT; 312 AA.
AC Q8N038;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate
transcarbamylase) (ATCase).
GN PYR OR C61612.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=1718;
RX [1]
SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspartate = phosphate
CC + N-carbamoyl-L-aspartate.
CC -1- PATHWAY: Pyrimidine biosynthesis; second step.
CC -1- SIMILARITY: Belongs to the ATCase/OTCase family.
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DR EMBL; AP005279; BAB99005.1; -.
DR HAMAP; MF_00001; -; 1.
DR InterPro; IPR006130; Asp/Om Cofact.
DR InterPro; IPR002082; Asp cardmltransf.
DR InterPro; IPR006131; OTCase_O.
DR InterPro; IPR006132; OTCase_P.
DR Pfam; PF00185; OTCase; 1.
DR Pfam; PF02729; OTCase; N; 1.
DR PRINTS; PR00100; AOTCASE.
DR TIGRPFAM; TIGR00670; asp_cab tr; 1.
```

DR PROSITE PS00097; CARBAMOYLTRANSFERRASE; 1.  
KM Pyrimidine biosynthesis; Transferrase; Complete proteome.  
SQ SEQUENCE 312 AA; 33894 MW; F33154F4D033CF22 CRC64;

Query Match 41.0%; Score 48; DB 1; Length 312;  
Best Local Similarity 61.1%; Pred. No. 3.7;  
Matches 11; Conservative 1; Mismatches 6; Indels 0; Gaps 0

OY 4 EILGRTGVLSNLRGT 21  
|:||||| |  
Db 27 EVLEGREVKKLPTLRGR 44

RESULT 9  
TSP3\_HUMAN ID TSP3\_HUMAN STANDARD; PRT; 956 AA.

AC PA9746; OBMV34;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Thrombospondin 3 precursor.  
GN THBS3 OR TSP3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=96044440; PubMed=7558000;  
RA Adolph K.W., Long G.L., Winfield S., Gimne E.I., Bernstein P.;  
RT "Structure and organization of the human thrombospondin 3 gene  
LTR";  
RL Genomics 27:329-336(1995).

RN [2]  
RP SEQUENCE OF 1-736 FROM N.A.  
RX MEDLINE=97474796; PubMed=9331372;  
RA Winfield S.L., Tayehi N., Martin B.M., Gimne E.I., Sidransky E.;  
RT "Identification of three additional genes contiguous to the  
glucocorticoid-inducible locus on chromosome 1q21: implications for Gaucher  
disease.";  
RL Genome Res. 7:1020-1026(1997).

RN [3]  
RP SEQUENCE OF 365-956 FROM N.A.  
RC TISSUE=Retina;  
RX MEDLINE=92388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.N., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schefer C.F., Bat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
Diatchenko L., Marushka K., Farmer A.A., Rubin G.M., Hong L.,  
Stepstone M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Ueda T.B., Toshiyuki S., Carrinci P., Prange C.T.,  
Rana S.S., Loquellano N.A., Peters G.U., Abramson R.D., Mullany S.J.,  
Boesch S.A., McWeeney P.J., McKernan K.O., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
Villalon D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
Rauber J.A., Krzyzanski M.I., Skalski U., Smallius D.E.,  
Schuerch A.V., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -1- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and  
cell-to-matrix interactions. Can bind to fibrinogen, fibronectin,  
laminin and type V collagen.  
CC -1- SUBUNIT: Oligomer; disulfide-linked.  
CC -1- SIMILARITY: Belongs to the thrombospondin family.  
CC -1- SIMILARITY: Contains 4 EGF-like domains.  
CC -1- SIMILARITY: Contains 7 TSP type-3 domains.

```
CC CC -I SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
CC -----
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CC -----
DR DR EMBL; L38969; AAC41762.1; -.
DR EMBL; AF023268; AAC51818.1; -.
DR EMBL; BC018786; AAH18786.1; -.
DR PIR; A57121; A57121.
DR HSSP; P35555; IEMN.
DR Genew; HGNC:11787; THBS3.
MIM; 188062; -.
DR GO; GO:0005509; F:calcium ion binding; TAS.
DR GO; GO:007150; P:cell-matrix adhesion; TAS.
DR InterPro; IPRO01881; EGF_Ca.
DR InterPro; IPRO06209; EGF_Like.
DR InterPro; IPRO03367; tsp_3.
DR InterPro; IPRO08859; TSPC.
DR InterPro; IPRO03129; TSPN.
DR Pfam; PF00008; EGF_1.
DR Pfam; PF02412; tsp_3; 13.
DR Pfam; PF05735; TSPC; 1.
DR Pfam; PF02210; TSPN; 1.
DR SMART; SMO0179; EGF_CA; 1.
DR SMART; SMO0210; TSPN; 1.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01861; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 3.
DR PROSITE; PS0187; EGF_CA; 2.
KW Glycoprotein; Cell adhesion; Calcium-binding; Repeat;
KW EGF-like domain; Signal.
FT SIGNAL. 1 21 POTENTIAL.
FT CHAIN 22 956 N-TERMINAL.
FT DOMAIN 22 272 THROMBOSPONDIN 3.
FT DOMAIN 274 315 EGF-LIKE 1.
FT DOMAIN 316 369 EGF-LIKE 2.
FT DOMAIN 370 413 EGF-LIKE 3.
FT DOMAIN 414 456 EGF-LIKE 4.
FT DOMAIN 488 523 TSP TYPE-3 1.
FT DOMAIN 524 546 TSP TYPE-3 2.
FT DOMAIN 547 582 TSP TYPE-3 3.
FT DOMAIN 583 605 TSP TYPE-3 4.
FT DOMAIN 606 643 TSP TYPE-3 5.
FT DOMAIN 644 683 TSP TYPE-3 6.
FT DOMAIN 684 719 TSP TYPE-3 7.
FT C-TERMINAL.
FT DOMAIN 720 956 INTERCHAIN (PROBABLY).
FT DISULFID 266 266 INTERCHAIN (PROBABLY).
FT DISULFID 269 269 INTERCHAIN (PROBABLY).
FT DISULFID 278 289 BY SIMILARITY.
FT DISULFID 283 300 BY SIMILARITY.
FT DISULFID 303 314 BY SIMILARITY.
FT DISULFID 320 332 BY SIMILARITY.
FT DISULFID 326 341 BY SIMILARITY.
FT DISULFID 344 368 BY SIMILARITY.
FT DISULFID 374 388 BY SIMILARITY.
FT DISULFID 382 397 BY SIMILARITY.
FT DISULFID 400 412 BY SIMILARITY.
FT DISULFID 418 432 BY SIMILARITY.
FT DISULFID 426 442 BY SIMILARITY.
FT DISULFID 444 455 BY SIMILARITY.
FT DISULFID 471 478 BY SIMILARITY.
FT DISULFID 483 503 BY SIMILARITY.
FT DISULFID 519 539 BY SIMILARITY.
FT DISULFID 542 562 BY SIMILARITY.
FT DISULFID 578 598 BY SIMILARITY.
FT DISULFID 601 621 BY SIMILARITY.
FT DISULFID 639 659 BY SIMILARITY.
FT DISULFID 679 699 BY SIMILARITY.
```

FT DISULFID 715 936 BY SIMILARITY.  
 FT CARBOHYD 310 310 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 407 407 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 644 644 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 937 937 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 956 AA; 104201 MW; AE9B136DF0F5E58 CRC64;

Query Match 40.2%; Score 47; DB 1; Length 956;  
 Best Local Similarity 45.5%; Pred. No. 18;  
 Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 1 QVLEIGRTECVLSNLRGTR 22  
 Db 113 QOAGLADGRTHVLLRLRGPSR 134

RESULT 10  
 YS59\_ENTFA STANDARD; PRT; 58 AA.  
 ID YS59\_ENTFA  
 AC 0830C9;  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Probable tautomerase EF2859 (EC 5.3.2.-).  
 GN EF2859.  
 OS Enterococcus faecalis (Streptococcus faecalis).  
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
 OX NCBI\_TaxID=1351;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=V583 / ATCC 700802;  
 RX MEDLINE=22550857; PubMed=12663927;  
 RA Paulsen I.T., Benartzi L., Myers G.S.A., Nelson K.E., Seshadri R.,  
 Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,  
 Ravelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,  
 Daugherty S., DeBoy R.T., Durkin S., Kolonyak J., Madupu R., Nelson W.,  
 Ramothepan S., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,  
 Ravelin H., Ravelin D., Ketchum K.A., Dougherty B.A., Fraser C.M.,  
 "Role of mobile DNA in the evolution of vancomycin-resistant  
 Enterococcus faecalis.";  
 RT Science 299:2071-2074(2003).  
 RL -1- SIMILARITY: Belongs to the tautomerase family.

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 CC -----  
 CC DR EMBL; AE016956; AA082551.1; -.  
 CC DR TIGR; EF2859; -.  
 CC DR HAMAP; MF\_00718; -; 1.  
 CC DR InterPro; IPR004370; Taut.  
 CC DR Pfam; PF01361; Tautomerase; 1.  
 CC DR ProDom; PD404143; Taut; 1.  
 CC DR Isoemerase; Complete proteome.  
 CC FT INT MET 0  
 CC FT ACT SITE 1  
 CC FT SEQUENCE 58 AA; 6589 MW; PAE19A0C5D93CE4E CRC64;

Query Match 39.3%; Score 46; DB 1; Length 58;  
 Best Local Similarity 60.0%; Pred. No. 1.2;  
 Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 3 VELEIGRTECVLSNLRGTR 17  
 Db 5 VELEIGRTECVLSNLRGTR 19

RESULT 11  
 RS28\_KLULA

ID RS28\_KLULA STANDARD; PRT; 67 AA.  
 AC P33285;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE 40S ribosomal protein S28 (S33).  
 GN RPS28.  
 OS Kluyveromyces fragilis (Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.  
 OX NCBI\_TaxID=28985;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93127729; PubMed=1481571;  
 RA Hoekstra R., Ferreira P.M., Bootsman T.C., Mager W.H., Planta R.J.,  
 RT "Structure and expression of the ABF1-regulated ribosomal protein S33  
 gene in Kluyveromyces.";  
 RL Yeast 8:949-959(1992).  
 RL -1- SIMILARITY: Belongs to the S28E family of ribosomal proteins.

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 CC -----  
 CC DR EMBL; X69582; CAA49296.1; -.  
 CC DR KIR; S30005; S30005.  
 CC DR InterPro; IPR000289; Ribosomal\_S28e.  
 CC DR Pfam; PF01200; Ribosomal\_S28e; 1.  
 CC DR ProDom; PD005541; Ribosomal\_S28e; 1.  
 CC DR PROSITE; PS00961; RIBOSOMAL\_S28E; 1.  
 CC KM Ribosomal protein.  
 CC SQ SEQUENCE 67 AA; 7536 MW; ESF148312B08A131 CRC64;

Query Match 39.3%; Score 46; DB 1; Length 67;  
 Best Local Similarity 42.9%; Pred. No. 1.4;  
 Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 2 RVELEIGRTECVLSNLRGTR 22  
 Db 29 RVELEIGRTECVLSNLRGTR 49

RESULT 12  
 RS28\_KLULA STANDARD; PRT; 67 AA.  
 ID RS28\_KLULA  
 AC P33286;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 40S ribosomal protein S28 (S33).  
 GN RPS28.  
 OS Kluyveromyces fragilis (Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.  
 OX NCBI\_TaxID=4911;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CBS 6556;  
 RX MEDLINE=93127729; PubMed=1481571;  
 RA Hoekstra R., Ferreira P.M., Bootsman T.C., Mager W.H., Planta R.J.,  
 RT "Structure and expression of the ABF1-regulated ribosomal protein S33  
 gene in Kluyveromyces.";  
 RL Yeast 8:949-959(1992).  
 RL -1- SIMILARITY: Belongs to the S28E family of ribosomal proteins.

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 CC -----  
 DR EMBL; X69583; CAA94297.1; -.  
 DR PIR; S30006; S30006.  
 DR InterPro; IPR000289; Ribosomal\_S28e.  
 DR Pfam; PF01200; Ribosomal\_S28e; 1.  
 DR ProDom; PD005541; Ribosomal\_S28e; 1.  
 DR PROSITE; PS00961; RIBOSOMAL\_S28e; 1.  
 KW Ribosomal protein.  
 SQ SEQUENCE 67 AA; 7522 MW; E1E558353F18A131 CRC64;  
 Query Match 39.3%; Score 46; DB 1; Length 67;  
 Best Local Similarity 42.9%; Pred. No. 1.4;  
 Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
 Db 29 RVEFLIEDTTRITVNVKGPVR 49  
 QY 2 RVEFLIEDTTRITVNVKGPVR 22  
 DB 29 RVEFLIEDTTRITVNVKGPVR 49  
 RESULT 13  
 C128 MYCTU STANDARD; PRT; 489 AA.  
 AC Q59572;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Putative cytochrome P450 128 (EC 1.14.-.-).  
 GN CYP128 OR RVZ268C OR MTJ330 OR MTCY339.42 OR MB2291C.  
 OS Mycobacterium tuberculosis, and  
 OS Mycobacterium tuberculosis.  
 OS Bacteria; Actinobacteria; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 NCBI\_Taxid=1773, 1765;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=M.tuberculosis; STRAIN=H37RV;  
 RX MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,  
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holtz S.,  
 RA Hornsby T., Jagels K., Kiroh A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
 RA Sultson J.E., Taylor K., Whitehead S., Barrell B.G.;  
 RA "Deciphering the biology of Mycobacterium tuberculosis from the  
 RT complete genome sequence."  
 RL Nature 393:537-544(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;  
 RX MEDLINE=22206494; PubMed=12218036;  
 RA Fleisbichmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., Deboy R., Dodson R., Gwinn M., Haft D., Hickey E.,  
 RA Kolonay J.F., Nelson W.C., Mayhew L.A., Ermolenko M., Salzberg S.L.,  
 RA Delcher A., Ustebayraktar T., Weidman J., Khouri H., Gill J., Mikula A.,  
 RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;  
 RA "Whole-genome comparison of Mycobacterium tuberculosis clinical and  
 RT laboratory strains."  
 RL J. Bacteriol. 184:5479-5490(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=M.bovis; STRAIN=AF212/97;  
 RX MEDLINE=22709107; PubMed=12788972;  
 RA Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,  
 RA Pryor M., Dutfoy S., Grondin S., Lacroix C., Monsenpe C., Simon S.,  
 RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,  
 RA Pakhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;  
 RA "The complete genome sequence of Mycobacterium bovis."  
 RT Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: Belongs to the cytochrome P450 family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 DR EMBL; Z71163; CAB00967.1; -.  
 DR EMBL; AE007076; AAK46612.1; -.  
 DR EMBL; BX248342; CAD97152.1; -.  
 DR PIR; H70729; H70729.  
 DR HSSP; Q00441; IOKA.  
 DR TIGR; MT2330; -.  
 DR Tuberculist; RV2268C; -.  
 DR InterPro; IPR001128; Cytochrome\_P450.  
 DR Pfam; PF00067; P450; 1.  
 DR PRINTS; PR00385; P450.  
 DR PROSITE; PS00086; CYTOCHROME\_P450; 1.  
 KW Hypothetical protein; Oxidoreductase; Monooxygenase; Heme;  
 KW Transmembrane; Complete proteome.  
 FT TRANSMEM 207 227 POTENTIAL.  
 FT TRANSMEM 256 276 POTENTIAL.  
 FT TRANSMEM 315 335 POTENTIAL.  
 FT TRANSMEM 383 403 POTENTIAL.  
 FT METAL 435 435 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).  
 SQ SEQUENCE 489 AA; 5313 MW; 633F233CE03AD7A CRC64;  
 Query Match 39.3%; Score 46; DB 1; Length 489;  
 Best Local Similarity 47.6%; Pred. No. 13;  
 Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;  
 QY 2 RVEFLIEDTTRITVNVKGPVR 22  
 DB 458 RIEVEPPTWTNANLGLTR 478  
 RESULT 14  
 AMS2 SCHPO STANDARD; PRT; 697 AA.  
 ID \_AMS2 SCHPO  
 AC Q9P714; Q9P714;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE CENP-A multicopy suppressor protein 2.  
 GN AMS2 OR SPC290.04 OR SPC4F11.01.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomyces.  
 NCBI\_Taxid=4896;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=9712;  
 RX MEDLINE=21848401; PubMed=11859360;  
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,  
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
 RA Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,  
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
 RA Holtz S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,  
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovich E.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skelton J., Simmonds M., Squares S., Squares S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Voicockert G., Aert R., Roben J., Grynopriaz B.,  
 RA Mellens I., Vanstraelen E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,







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OM protein - protein search, using sw model

Run on: May 6, 2004, 12:44:02 / Search time 21 Seconds  
(without alignments)  
105.353 Million cell updates/sec

Title: US-10-612-885A-1

Perfect score: 117  
Sequence: 1 QRVLEIGRTECVLSNLGRTRY 23

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 117   | 100.0       | 508    | 1 ZUHUR  | erythropoietin rec |
| 2          | 109   | 93.2        | 265    | 2 S14081 | erythropoietin rec |
| 3          | 109   | 93.2        | 507    | 1 A32385 | erythropoietin rec |
| 4          | 109   | 93.2        | 507    | 1 A46713 | erythropoietin rec |
| 5          | 47    | 40.2        | 956    | 2 A57121 | thrombospondin 3 p |
| 6          | 46    | 39.3        | 67     | 2 S30006 | ribosomal protein  |
| 7          | 46    | 39.3        | 67     | 2 S30005 | ribosomal protein  |
| 8          | 46    | 39.3        | 288    | 2 T30648 | probable DNA-bind  |
| 9          | 46    | 39.3        | 489    | 1 H70729 | cytochrome P450 RV |
| 10         | 46    | 39.3        | 710    | 2 T41352 | probable transcrip |
| 11         | 46    | 39.3        | 1609   | 2 S44821 | F44E2.4 protein -  |
| 12         | 45.5  | 38.9        | 607    | 1 S42639 | ATP-dependent RNA  |
| 13         | 45    | 38.5        | 316    | 2 D83406 | probable transmem  |
| 14         | 45    | 38.5        | 512    | 1 D70506 | hypothetical prote |
| 15         | 45    | 38.5        | 1036   | 2 S22383 | axomin 1 precursor |
| 16         | 44.5  | 38.0        | 810    | 2 T44430 | protein PV100 [imp |
| 17         | 44    | 37.6        | 47     | 2 AB0673 | 30S ribosomal prot |
| 18         | 44    | 37.6        | 195    | 2 A51823 | hypothetical prote |
| 19         | 43    | 36.8        | 84     | 2 C97995 | degenerate transp  |
| 20         | 43    | 36.8        | 20     | 2 A87649 | hypothetical prote |
| 21         | 43    | 36.8        | 418    | 2 C95184 | IS1167, transpos   |
| 22         | 43    | 36.8        | 418    | 2 P95096 | IS1167, transpos   |
| 23         | 43    | 36.8        | 654    | 2 S67870 | hypothetical prote |
| 24         | 43    | 36.8        | 931    | 2 S65574 | transferrin-bind   |
| 25         | 43    | 36.8        | 956    | 1 A46016 | thrombospondin 3 - |
| 26         | 43    | 36.8        | 1437   | 2 T31053 | probable protein-t |
| 27         | 42.5  | 36.3        | 228    | 2 H71251 | hypothetical prote |
| 28         | 42.5  | 36.3        | 1894   | 2 C54689 | protein-tyrosine-p |
| 29         | 42.5  | 36.3        | 1912   | 2 A56178 | protein-tyrosine-p |

|    |    |      |     |          |                    |
|----|----|------|-----|----------|--------------------|
| 30 | 42 | 35.9 | 67  | 1 R3BY33 | ribosomal protein  |
| 31 | 42 | 35.9 | 67  | 2 S51401 | ribosomal protein  |
| 32 | 42 | 35.9 | 231 | 2 T49830 | hypothetical prote |
| 33 | 42 | 35.9 | 255 | 2 A97877 | transposase (orf2) |
| 34 | 42 | 35.9 | 260 | 2 C98084 | degenerate transp  |
| 35 | 42 | 35.9 | 283 | 2 S75226 | esterase, SL1916 - |
| 36 | 42 | 35.9 | 322 | 2 D89785 | hypothetical prote |
| 37 | 42 | 35.9 | 365 | 2 Q00198 | aspartate-semialde |
| 38 | 42 | 35.9 | 418 | 2 A95168 | IS1167, transpos   |
| 39 | 42 | 35.9 | 418 | 2 B95197 | IS1167, transpos   |
| 40 | 42 | 35.9 | 418 | 2 E95146 | IS1167, transpos   |
| 41 | 42 | 35.9 | 418 | 2 H95208 | IS1167, transpos   |
| 42 | 42 | 35.9 | 482 | 2 T46944 | thiamin biosynthes |
| 43 | 42 | 35.9 | 482 | 2 A10554 | thiamin biosynthes |
| 44 | 42 | 35.9 | 482 | 2 T29652 | inward rectifier p |
| 45 | 42 | 35.9 | 562 | 2 E70399 | hydrogenase regula |

## ALIGNMENTS

## RESULT 1

ZUHUR  
erythropoietin receptor precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 12-Feb-1993 #sequence, revision 05-Apr-1995 #text change 22-Jun-1999  
C:Accession: A43799; A60160; A49824; A53958; A55280; J52563  
R:Jones, S.S.; D'Andrea, A.D.; Haines, L.L.; Wong, G.G.  
Blood 76, 31-35, 1990  
A:Title: Human erythropoietin receptor: cloning, expression, and biologic characterization  
A:Accession: A43799; MUID:90304340; PMID:2163696  
A:Molecule type: mRNA  
A:Residues: 1-508 <JON>  
A:Cross-references: GB:M60459; NID:G182244; PIDN:AAA52403.1; PID:G182245  
R:Winkelmann, J.C.; Penny, L.A.; Deaven, L.L.; Forget, B.G.; Jenkins, R.B.  
Blood 76, 24-30, 1990  
A:Title: The gene for the human erythropoietin receptor: analysis of the coding sequence  
A:Reference number: A60160; MUID:90304334; PMID:2163695  
A:Accession: A60160  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA; DNA  
A:Residues: 1-101, 'R', 103-188, 'RP', 191-243, 'E', 245-508 <WIN>  
R:Noguchi, C.T.; Bae, K.S.; Chin, K.; Wada, Y.; Schechter, A.N.; Hankins, W.D.  
Blood 76, 2548-2556, 1991  
A:Title: Cloning of the human erythropoietin receptor gene.  
A:Reference number: A49824; MUID:92399733; PMID:1668606  
A:Accession: A49824  
A:Molecule type: DNA  
A:Residues: 1-508 <NOG>  
A:Cross-references: GB:S45332; NID:G255496; PIDN:AAA23271.1; PID:G255497  
A:Experimental source: Placenta  
A>Note: sequence extracted from NCBI backbone (NCBIN:113293, NCBIPI:113294)  
R:Ehnenman, K.; St. John, T.  
Exp. Hematol. 19, 973-977, 1991  
A:Title: The erythropoietin receptor gene: cloning and identification of multiple trans  
A:Reference number: A53958; MUID:91372359; PMID:1654273  
A:Accession: A53958  
A:Molecule type: mRNA  
A:Residues: 1-508 <EHR>  
R:Penny, L.A.; Forget, B.G.  
Genomics 11, 974-980, 1991  
A:Title: Genomic organization of the human erythropoietin receptor gene.  
A:Reference number: A55280; MUID:92147143; PMID:1664413  
A:Accession: A55280  
A:Molecule type: DNA  
A:Residues: 1-17,381-387, 'LPEQOQDA', 391-395,504-508 <PEN>  
A>Note: sequence modified after extraction from NCBI backbone  
A>Note: the authors translated the codon GAT for residue 31 as B  
R:Mauche, L.; Touramille, C.; Hatlab, C.; Boffa, G.; Cartton, J.P.; Chretien, S.  
Blood 76, 2557-2563, 1991  
A:Title: Cloning of the gene encoding the human erythropoietin receptor.

A:Reference number: I52563; MUID:92399734; PMID:1668607  
A:Accession: I52563  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-96 <RES>  
A:Cross-references: GB:M76595; NID:g182147; PIDN:AAA52393.1; PID:g553281  
C:Genetic:  
A:Gene: GDB:EPOR  
A:Cross-references: GDB:125242; OMIM:133171  
A:Map position: 19p13.3-19p13.2  
A:Insertions: 39/1; 84/2; 143/1; 195/3; 247/1; 276/2; 305/3  
C:Superfamily: erythropoietin receptor; cytokine receptor homology  
C:Keywords: alternative splicing; cytokine receptor; glycoprotein;  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-508/Product: erythropoietin receptor #status predicted <MAT>  
F:52-250/Domain: extracellular #status predicted <EXT>  
F:52-239/Domain: cytokine receptor homology <CRS>  
F:233-237/Region: WSXWS motif  
F:251-272/Domain: transmembrane #status predicted <TM>  
F:273-508/Domain: intracellular #status predicted <INT>  
F:52-62,91-107/Disulfide bonds: #status predicted  
F:75/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 100.0%; Score 117; DB 1; Length 508;  
Best Local Similarity 100.0%; Pred. No. 2.6e-10;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ORVEILEGRTECVLSNLRGTRY 23  
Db 194 QRAVELEGRTECVLSNLRGTRY 216  
|||||

RESULT 2  
S14081  
erythropoietin receptor - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S14081; I49653  
R:Kuramochi, S.; Ikawa, Y.; Todokoro, K.  
J. Mol. Biol. 216, 567-575, 1990  
A:Title: Characterization of murine erythropoietin receptor genes.  
A:Reference number: S13249; MUID:91080149; PMID:2175360  
A:Accession: S14081  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-265 <KUR>  
R:LeCombe, C.; Chretien, S.; Lemarchandel, V.; Mayeux, P.; Romeo, P.  
J. Biol. Chem. 266, 6952-6956, 1991  
A:Title: Spleen focus-forming virus long terminal repeat insertional activation of the m  
A:Reference number: I49653; MUID:91201346; PMID:1849897  
A:Accession: I49653  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-24 <RES>  
A:Cross-references: GB:M62360; NID:g193199; PIDN:AAA37582.1; PID:g193200  
C:Superfamily: erythropoietin receptor; cytokine receptor homology  
C:Keywords: cytokine receptor; transmembrane protein  
F:52-238/Domain: cytokine receptor homology <CRS>

Query Match 93.2%; Score 109; DB 2; Length 265;  
Best Local Similarity 91.3%; Pred. No. 2.3e-09;  
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ORVEILEGRTECVLSNLRGTRY 23  
Db 193 QRAVELEGRTECVLSNLRGTRY 215  
|||||

RESULT 3  
A32385  
erythropoietin receptor precursor, membrane-bound form - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 28-Sep-1990 #sequence\_revision 05-Apr-1995 #text\_change 22-Jun-1999

C:Accession: A41686; A32385; S13249  
R:Hino, M.; Tojo, A.; Misawa, Y.; Morii, H.; Takaku, F.; Shibuya, M.  
Mol. Cell. Biol. 11, 5527-5533, 1991  
A:Title: Unregulated expression of the erythropoietin receptor gene caused by insertion <

A:Reference number: A41686; MUID:92017832; PMID:1656233  
A:Accession: A41686  
A:Molecule type: mRNA  
A:Residues: 1-507 <HIN>  
A:Cross-references: GB:S59388; NID:g237036; PIDN:AAB20029.1; PID:g237037  
A:Experimental source: murine erythroleukemia (MEL) cell line F5-5  
R:D'Andrea, A.D.; Iodish, H.F.; Wong, G.G.  
Cell 57, 277-285, 1989

A:Title: Expression cloning of the murine erythropoietin receptor.  
A:Reference number: A32385; MUID:89195238; PMID:2519263  
A:Accession: A32385  
A:Molecule type: mRNA

A:Residues: 1-507 <DNA>  
A:Cross-references: GB:U04843; NID:g193090; PIDN:AAA37571.1; PID:g309219  
A:Experimental source: murine erythroleukemia (MEL) cells, subclone 745  
R:Kuramochi, S.; Ikawa, Y.; Todokoro, K.  
J. Mol. Biol. 216, 567-575, 1990

A:Title: Characterization of murine erythropoietin receptor genes.  
A:Reference number: S13249; MUID:91080149; PMID:2175360  
A:Accession: S13249  
A:Molecule type: DNA; mRNA  
A:Residues: 1-507 <KUR>  
A:Cross-references: EMBL:X53081; NID:g50861; PIDN:CAA37248.1; PID:g50862  
A:Experimental source: murine erythroleukemia K-1 cells

C:Genetic:  
A:Insertions: 39/1; 83/2; 142/1; 194/3; 246/1; 276/2; 304/3  
C:Superfamily: erythropoietin receptor; cytokine receptor homology  
C:Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-507/Product: erythropoietin receptor #status predicted <MAT>  
F:52-249/Domain: extracellular #status predicted <EXT>  
F:52-238/Domain: cytokine receptor homology <CRS>  
F:250-271/Domain: transmembrane #status predicted <TM>  
F:272-507/Domain: intracellular #status predicted <INT>  
F:52-62,90-106/Disulfide bonds: #status predicted  
F:75/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 93.2%; Score 109; DB 1; Length 507;  
Best Local Similarity 91.3%; Pred. No. 4.6e-09;  
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ORVEILEGRTECVLSNLRGTRY 23  
Db 193 QRAVELEGRTECVLSNLRGTRY 215  
|||||

RESULT 4  
A46713  
erythropoietin receptor precursor - rat  
C:Species: Rattus norvegicus (Norway Rat)  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Jun-2000  
C:Accession: A46713  
R:Masuda, S.; Nago, M.; Takahata, K.; Konishi, Y.; Gallyas Jr., F.; Tabira, T.; Sasaki, J.  
J. Biol. Chem. 268, 11208-11216, 1993  
A:Title: Functional erythropoietin receptor of the cells with neural characteristics. Com  
A:Reference number: A46713; MUID:9326574; PMID:7664373  
A:Accession: A46713  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-507 <MAS>  
A:Cross-references: GB:D13566; NID:g286209; PIDN:BA02761.1; PID:g286210  
A:Experimental source: PC12 and erythroid cells  
A:Note: Sequence extracted from NCBI backbone (NCBIN:132811, NCBI:P:132813)  
C:Superfamily: erythropoietin receptor; cytokine receptor homology  
C:Keywords: cytokine receptor; glycoprotein; transmembrane protein  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-507/Product: erythropoietin receptor #status predicted <MAT>  
F:25-249/Domain: extracellular #status predicted <EXT>  
F:52-238/Domain: cytokine receptor homology <CRS>

F:250-271/Domain: transmembrane #status predicted <TM>  
 F:272-507/Domain: intracellular #status predicted <INT>  
 F:75/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 93.2%; Score 109; DB 1; Length 507;  
 Best Local Similarity 91.3%; Pred. No. 4.6e-09;  
 Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QRVLELGRTECVLSNLRGRTY 23  
 DB 193 QRVLELGRTECVLSNLRGRTY 215

## RESULT 5

A57121  
 Chromobospondin 3 precursor - human

C/Species: Homo sapiens (man)  
 C/Date: 03-Nov-1995 #sequence\_revision 03-Nov-1995 #text\_change 21-Jan-2000

C/Accession: A57121; T08830  
 R/Adolph, K.W.; Long, G.L.; Winfield, S.; Glines, E.I.; Bornstein, P.

Genomics 27, 329-336, 1995  
 A/Title: Structure and organization of the human chromobospondin 3 gene (THBS3).

A/Reference number: A57121; MUID:96044440; PMID:7558000

A/Accession: A57121

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-956 <ADO>  
 A/Cross-references: GB:L38969; NID:g886298; PIDN:AAC41762.1; PID:g886299; GB:L38970

R/Winfield, S.L.; Tayebi, N.; Martin, B.M.; Glines, E.I.; Sidransky, E.  
 Genome Res. 7, 1020-1026, 1997

A/Title: Identification of three additional genes contiguous to the glucocerebrosidase 1  
 A/Reference number: Z16482; MUID:97474796; PMID:9331372

A/Accession: T08830

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-736 <WIN>

A/Cross-references: EMBL:AF023268; NID:g2564910; PIDN:AAC51818.1; PID:g2564912

C/Genetics:

A/Gene: GDB:THBS3

A/Cross-references: GDB:409953; OMIM:188062

A/Map position: 1921-1923

A/Intons: 27/1; 96/1; 181/3; 216/1; 225/1; 256/1; 270/1; 319/3; 366/3; 392/3; 443/3; 48

C/Function: mediates cell-to-matrix and cell-to-cell interactions

A/Superfamily: chromobospondin 3; EGF homology

F:374-412/Domain: EGF homology <EGF>

Query Match 40.2%; Score 47; DB 2; Length 956;  
 Best Local Similarity 45.5%; Pred. No. 41;  
 Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QRVLELGRTECVLSNLRGRTY 22  
 DB 113 QQAGLADGRTRTVLRLRGPR 134

RESULT 6  
 S30006  
 ribosomal protein S28.e - Yeast (Kluyveromyces marxianus)

N/Alternate names: ribosomal protein Y53  
 C/Species: Kluyveromyces marxianus

C/Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 07-May-1999

C/Accession: S30006  
 R/Hoekstra, R.; Ferreira, P.M.; Bootsman, T.C.; Mager, W.H.; Planta, R.J.

Yeast 8, 949-959, 1992  
 A/Title: Structure and expression of the ABP1-regulated ribosomal protein S33 gene in Kl

A/Reference number: S30005; MUID:99127729; PMID:1481571

A/Accession: S30006  
 A/Molecule type: DNA  
 A/Residues: 1-67 <HOB>  
 A/Cross-references: GB:S52656  
 C/Genetics:  
 A/Gene: S33

C/Superfamily: rat ribosomal protein S28  
 C/Keywords: protein biosynthesis; ribosome

Query Match 39.3%; Score 46; DB 2; Length 67;  
 Best Local Similarity 42.9%; Pred. No. 3.7;  
 Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 RVELELGRTECVLSNLRGRTY 22  
 DB 29 RVELELGRTECVLSNLRGRTY 49

## RESULT 7

S30005  
 ribosomal protein S28.e - Yeast (Kluyveromyces marxianus var. lactis)

N/Alternate names: ribosomal protein Y53  
 C/Species: Kluyveromyces marxianus var. lactis; Candida spherica

C/Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 07-May-1999

C/Accession: S30005  
 R/Hoekstra, R.; Ferreira, P.M.; Bootsman, T.C.; Mager, W.H.; Planta, R.J.

Yeast 8, 949-959, 1992  
 A/Title: Structure and expression of the ABP1-regulated ribosomal protein S33 gene in Kl

A/Reference number: S30005; MUID:93127729; PMID:1481571

A/Accession: S30005

A/Molecule type: DNA

A/Residues: 1-67 <HOB>

A/Cross-references: GB:S53420

C/Genetics:

A/Gene: S33

C/Superfamily: rat ribosomal protein S28

C/Keywords: protein biosynthesis; ribosome

Query Match 39.3%; Score 46; DB 2; Length 67;  
 Best Local Similarity 42.9%; Pred. No. 3.7;  
 Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 RVELELGRTECVLSNLRGRTY 22  
 DB 29 RVELELGRTECVLSNLRGRTY 49

RESULT 8  
 T30648  
 probable DNA-binding protein 46L - Moluscum contagiosum virus 1

N/Alternate names: MC046L  
 C/Species: Moluscum contagiosum virus 1

C/Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 27-Oct-2003

C/Accession: T30648

R/Senkevich, T.G.; Bugert, J.U.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.

Science 273, 813-816, 1996  
 A/Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host re

A/Reference number: Z20876; MUID:96325459; PMID:8670425

A/Accession: T30648

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-288 <SEN>

A/Cross-references: EMBL:U60315; NID:g1491943; PIDN:AAC55174.1; PID:g1491989

C/Genetics:

A/Note: MC046L

C/Superfamily: DNA-binding phosphoprotein, vaccinia 13L type

C/Keywords: DNA binding

Query Match 39.3%; Score 46; DB 2; Length 288;  
 Best Local Similarity 66.7%; Pred. No. 17;  
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 11 ECVLSNLRGRTY 22  
 DB 133 ECVLSNLRGRTY 144

## RESULT 9

H70729



QY 2 RVEILEGRTECVLSNLGRRTY 23  
 DB 195 RVALVAGRVE--LSPLHGRGRW 214

## RESULT 14

D70506  
 hypothetical protein Rv2733c - Mycobacterium tuberculosis (strain H37Rv)  
 C/Species: Mycobacterium tuberculosis  
 C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000  
 C/Accession: D70506  
 R/Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998  
 A/Authors: Sgarbes, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
 A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
 A/Reference number: A70500; MUID:98295987; PMID:9634230  
 A/Accession: D70506  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-512 <COL>  
 A/Cross-references: GB:298209; GB:AL123456; NID:G3261838; PIDN:CAB10909.1; PID:G2292967  
 A/Experimental source: strain H37Rv  
 C/Genetics:  
 A/Gene: Rv2733c  
 C/Superfamily: conserved hypothetical protein b0835

Query Match 38.5%; Score 45; DB 1; Length 512;  
 Best Local Similarity 42.3%; Pred. No. 44;  
 Matches 11; Conservative 4; Mismatches 7; Indels 4; Gaps 1;

QY 1 QRVETL---EGRTCEVLSNLGRTR 22  
 DB 408 QAVEVLVATGGRKDTVTARMSGRAR 433

## RESULT 15

S22383  
 axonin 1 precursor - chicken  
 N/Alternate names: neural cell adhesion molecule AxCAM  
 C/Species: Gallus gallus (chicken)  
 C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
 C/Accession: S22383; S34107; S69332; S22128  
 R/Zuellig, R.A.; Rader, C.; Schroeder, A.; Kalousek, M.B.; von Bohlen und Halbach, F.; C  
 Eur. J. Biochem. 204, 453-463, 1992  
 A/Title: The axonally secreted cell adhesion molecule, axonin-1. Primary structure, immu  
 A/Reference number: S22383; MUID:92174898; PMID:1311675  
 A/Accession: S22383  
 A/Molecule type: mRNA  
 A/Residues: 1-1036 <ZUE1>  
 A/Cross-references: EMBL:X63101; NID:G62852; PIDN:CAA44815.1; PID:G62853  
 A/Accession: S34107  
 A/Molecule type: protein  
 A/Residues: 29-49;51-80;84-95;100-117;120-128;130-141;143-176;243-254;256-296;303-336;33  
 R/Giger, R.U.; Vogt, L.; Zuellig, R.A.; Rader, C.; Hennehan-Beatty, A.; Wolfer, D.P.; Sch  
 Eur. J. Biochem. 227, 617-628, 1995  
 A/Title: The gene of chicken axonin-1. Complete structure and analysis of the promoter.  
 A/Reference number: S69332; MUID:95172044; PMID:7867620  
 A/Accession: S69332  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1002-1036 <GIG>  
 A/Cross-references: EMBL:X79607  
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994  
 C/Superfamily: contactin; fibronectin type III repeat homology; immunoglobulin homology  
 C/Keywords: cell adhesion  
 F/1-23/Domain: signal sequence #status predicted <SIG>  
 F/24-1036/Product: axonin 1 #status predicted <MAT>  
 F/336-392/Domain: immunoglobulin homology <IMM>

Query Match 38.5%; Score 45; DB 2; Length 1036;

Best Local Similarity 47.1%; Pred. No. 92;  
 Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 7 EGRTCEVLSNLGRRTY 23  
 DB 296 EGYECCAEENIKGRDYY 312

Search completed: May 6, 2004, 12:47:27  
 Job time : 22 secs

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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: May 6, 2004, 12:38:56 ; Search time 54 Seconds  
(without alignments)  
120.344 Million cell updates/sec

Title: US-10-612-885A-1

Perfect score: 117  
Sequence: 1 QRVFELLEGRECTVLSNLRGRTRY 23Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

1: geneseqp1980s:\*\n2: geneseqp1990s:\*\n3: geneseqp2000s:\*\n4: geneseqp2001s:\*\n5: geneseqp2002s:\*\n6: geneseqp2003as:\*\n7: geneseqp2003bs:\*\n8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 117   | 100.0       | 23     | AAV39411 | AAV39411 Human ery |
| 2          | 117   | 100.0       | 23     | AAU78011 | AAU78011 Human ery |
| 3          | 117   | 100.0       | 23     | ABP72837 | ABP72837 Erythrocy |
| 4          | 117   | 100.0       | 30     | AA98938  | AA98938 Synthetic  |
| 5          | 117   | 100.0       | 211    | AA821686 | AA821686 Human mat |
| 6          | 117   | 100.0       | 225    | AA821685 | AA821685 Human mat |
| 7          | 117   | 100.0       | 438    | AAV44622 | AAV44622 Truncated |
| 8          | 117   | 100.0       | 438    | AAV44623 | AAV44623 R154C tru |
| 9          | 117   | 100.0       | 458    | ADE28671 | ADE28671 Human NOV |
| 10         | 117   | 100.0       | 458    | ADE28673 | ADE28673 Human NOV |
| 11         | 117   | 100.0       | 458    | ADE28675 | ADE28675 Human NOV |
| 12         | 117   | 100.0       | 488    | AAW08349 | AAW08349 EPOReC fu |
| 13         | 117   | 100.0       | 503    | AA813012 | AA813012 O-tagged  |
| 14         | 117   | 100.0       | 508    | AA806512 | AA806512 EPO recep |
| 15         | 117   | 100.0       | 508    | AA847518 | AA847518 Human EPO |
| 16         | 117   | 100.0       | 508    | AA870032 | AA870032 Human ery |
| 17         | 117   | 100.0       | 508    | AA869503 | AA869503 Human ery |
| 18         | 117   | 100.0       | 508    | AB809173 | AB809173 Human ery |
| 19         | 111   | 94.9        | 508    | ADE28677 | ADE28677 Human NOV |
| 20         | 109   | 93.2        | 265    | AA830326 | AA830326 Mouse sol |
| 21         | 109   | 93.2        | 507    | AA806511 | AA806511 EPO recep |
| 22         | 109   | 93.2        | 507    | AA847517 | AA847517 MEL EPO r |
| 23         | 109   | 93.2        | 507    | AA869502 | AA869502 Mouse ery |
| 24         | 102   | 87.2        | 507    | AA850327 | AA850327 Mouse sol |
| 25         | 52    | 44.4        | 1026   | AA80379  | AA80379 Human BIG  |

|    |    |      |      |   |          |                    |
|----|----|------|------|---|----------|--------------------|
| 26 | 52 | 44.4 | 1028 | 2 | AAW29667 | AAW29667 Homo sapi |
| 27 | 49 | 41.9 | 49   | 4 | AA884225 | AA884225 A tumour  |
| 28 | 49 | 41.9 | 49   | 5 | AA813249 | AA813249 Human tum |
| 29 | 49 | 41.9 | 199  | 4 | ABG13674 | ABG13674 Novel hum |
| 30 | 49 | 41.9 | 221  | 5 | ABP65639 | ABP65639 Bifidobac |
| 31 | 49 | 41.9 | 286  | 5 | ABP43791 | ABP43791 Human Krl |
| 32 | 49 | 41.9 | 321  | 2 | AAV02136 | AAV02136 Protein e |
| 33 | 49 | 41.9 | 341  | 4 | AA897378 | AA897378 Human Krl |
| 34 | 49 | 41.9 | 373  | 3 | AA866034 | AA866034 Human TAN |
| 35 | 49 | 41.9 | 373  | 6 | ABO32694 | ABO32694 Secreted  |
| 36 | 49 | 41.9 | 413  | 4 | AA884220 | AA884220 A human t |
| 37 | 49 | 41.9 | 413  | 5 | AA813244 | AA813244 Human tum |
| 38 | 49 | 41.9 | 451  | 4 | AA866063 | AA866063 Murine pr |
| 39 | 49 | 41.9 | 451  | 6 | ABO32717 | ABO32717 Secreted  |
| 40 | 49 | 41.9 | 456  | 4 | AA866033 | AA866033 Human TAN |
| 41 | 49 | 41.9 | 456  | 6 | ABO32693 | ABO32693 Secreted  |
| 42 | 49 | 41.9 | 458  | 2 | AAV02135 | AAV02135 HTB8247 P |
| 43 | 49 | 41.9 | 458  | 5 | ABG76512 | ABG76512 DNA encod |
| 44 | 49 | 41.9 | 470  | 4 | AA866083 | AA866083 Murine TA |
| 45 | 49 | 41.9 | 470  | 6 | ABU08371 | ABU08371 Amino aci |

## ALIGNMENTS

RESULT 1  
AAV39411  
ID AAV39411 standard; peptide; 23 AA.

AC AAV39411;  
DT 30-NOV-1999 (first entry)

DE Human erythropoietin receptor-derived activation peptide.

KW Erythropoietin; EPO; receptor; activation; internalisation.

OS Synthetic.

PS Homo sapiens.

PN WO9942127-A2.

PD 26-AUG-1999.

PF 23-FEB-1999; 99WO-US003910.

PR 24-FEB-1998; 98US-00028938.

PA (RECE-) RECEPTRON INC.

PI Olsson L, Naranda T;

DR WPI; 1999-527422/44.

PT Modulating activity of type-2 cell surface receptors used in treatment  
of, e.g. Obesity.

PS Claim 8; Page 17; 92pp; English.

This sequence represents a peptide derived from the extracellular activation sequence of the human erythropoietin (EPO) receptor. Activation sequences are involved in modulation of receptor responses and are separate from the ligand binding site. Activation sequences are important in two distinct ways: in the modulation of receptor internalisation; and/or in the modulation of activation sequence of the receptor. Use of peptides corresponding to the activation sequence of a receptor can retard or inhibit receptor internalisation, thereby increasing or stabilising the steady-state number of active receptors on the cell surface. This has the effect of increasing signalling per unit of ligand. In addition, the receptor is classed as a type 2 cell surface receptor, meaning that such peptides can actually replace the requirement for the ligand, causing ligand-independent activation. This activation is probably brought about by a dimerisation mechanism in which one peptide

CC molecule is bound by two receptors, mimicking the dimerisation and  
CC subsequent activation that occurs when two receptors bind one ligand.  
CC This peptide could be used to treat disorders involving an inadequate or  
CC inappropriate response from its corresponding receptor

XX Sequence 23 AA;

Query Match 100.0%; Score 117; DB 2; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3.6e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRVETLEGRTECVLSNLRGRTRY 23  
ID 1 QRVETLEGRTECVLSNLRGRTRY 23

RESULT 2  
AAU78011  
ID AAU78011 standard; peptide; 23 AA.

XX AAU78011;

DT 05-JUN-2002 (first entry)

XX Human erythropoietin receptor activation domain oligopeptide.

XX Erythropoietin receptor; antidiabetic; activation sequence; ligand;  
KM receptor internalisation; type 2 diabetes; drug screening; human.

XX Homo sapiens.

XX US6333031-B1.

XX 25-DEC-2001.

XX 24-FEB-1998; 98US-00028937.

XX 08-MAR-1996; 96US-00612999.

XX 22-AUG-1996; 96US-00701382.

XX 23-JAN-1997; 97US-00788820.

XX (RECE-) RECEPTRON INC.

XX Olsson L, Naranda T;

XX WPI; 2002-224899/28.

XX Composition comprising peptides from receptor extracellular domains,  
PT useful for e.g. modulating receptor internalization and activation such  
PT as increasing insulin activity.

XX Claim 1; Col 11; 48pp; English.

XX This invention corresponds to a novel composition comprising any of 34

XX peptides consisting of activation sequences from the extracellular

XX domains of cell-surface receptors. These peptides were identified by

XX homology searching with a peptide sequence from the MHC class I alpha I

XX domain and correspond to the activation sequences of the associated

XX receptor. Activation sequences are involved in the internalisation of

XX receptors and so these peptides may be used to modulate the

XX internalisation and or activation of these receptors. The peptides of the

XX invention may also be used to increase effect of ligand signalling in

XX type 2 diabetes and can replace the ligand normally required for

XX activation. This is useful when the ligand is a hormone and is difficult

XX to obtain. The peptides may also interact synergistically with the ligand

XX or function as antagonists of receptor signalling. The peptides can also

XX be used in drug screening to identify compounds that modulate receptor

XX internalisation or function as ligand replacements. Use of these peptides

XX can increase the effect of therapeutic hormones (optionally co-

XX administered) by at least 50% and are specific for the receptors from

XX which they derive. The present sequence represents the human

XX Erythropoietin receptor activation sequence oligopeptide of the invention

SQ Sequence 23 AA;

Query Match 100.0%; Score 117; DB 5; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3.6e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRVETLEGRTECVLSNLRGRTRY 23  
ID 1 QRVETLEGRTECVLSNLRGRTRY 23

RESULT 3  
ABP72837  
ID ABP72837 standard; peptide; 23 AA.

XX ABP72837;

DT 11-AUG-2003 (first entry)

XX Erythropoietin mimetic peptide.

XX Transferrin; neuroprotective; cerebroprotective; vasotropic;  
KM antiparkinsonian; nootropic; anti-HIV; antiaesthetic; antiallergic;  
KM cytostatic; immunosuppressive; antithrombotic; cardiac;

KM gynaecological; immunostimulant; antianaemic; haemostatic;  
KM antiinflammatory; dermatological; antibacterial; virucide; antiparasitic;

KM fungicide; hepatotropic; antirheumatic; antiarthritic; antigout;  
KM tranquilizer; vulnery; antidiabetic; nephrotropic; antipyretic;

KM gastrointestinal; gene therapy; transgenic animal; erythropoietin;  
KM mimetic; agonist.

XX Synthetic.

XX WO2003020746-A1.

XX 13-MAR-2003.

XX 30-AUG-2002; 2002WO-US027637.

XX 30-AUG-2001; 2001US-0315745P.

XX 30-NOV-2001; 2001US-0334059P.

XX (BIOR-) BIOREXIS PHARM CORP.

XX Prior CP;

XX WPI; 2003-332916/31.

XX New fusion protein, useful in the diagnosis and treatment of diseases or

XX disorders relating to the respiratory, cardiovascular and digestive

XX systems, comprises a transferrin protein fused to a therapeutic protein.

XX Example 9; Page 255; 298pp; English.

XX The present sequence is that of an erythropoietin (EPO) mimetic peptide

XX which has no homology to natural EPO but has similar biological

XX properties in that it activates the EPO receptor acting as an agonist.

XX The EPO mimetic peptide can be included in novel fusion proteins of the

XX invention also including a transferrin (Tf, see ABP72837) moiety

XX engineered to extend the serum half-life or bioavailability. The EPO

XX mimetic peptide can be fused to the N- or C-terminus of Tf, or inserted

XX into, or used to replace part of Tf, such that the Tf acquires EPO

XX activity. Modified Tf fusion proteins of the invention can be used in the

XX diagnosis, prognosis, prevention and/or treatment of diseases and/or

XX disorders of the endocrine, nervous, immune, respiratory, cardiovascular,

XX reproductive and digestive systems, diseases and/or disorders relating to

XX the blood or to cell proliferation, inflammatory conditions and

XX infectious diseases, or to deliver a therapeutic agent to a cell or

XX across the blood-brain barrier

XX Sequence 23 AA;

Query Match 100.0%; Score 117; DB 6; Length 23;



Best Local Similarity 100.0%; Pred. No. 3.6e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QRVETLEGRTCVLSNLRGRTRY 23  
DB 1 QRVETLEGRTCVLSNLRGRTRY 23

## RESULT 4

AAR98938  
ID AAR98938 standard; peptide; 30 AA.

XX AAR98938;

XX 28-SEP-1996 (first entry)

XX Synthetic human erythropoietin receptor peptide, SE-8.

XX Monoclonal antibody; erythropoietin receptor; diagnosis; anaemia;

XX erythropoiesis; erythrocyte production; epitope mapping.

XX Synthetic.

XX WO9603438-A1.

XX 08-FEB-1996.

XX 26-JUL-1995; 95WO-US009458.

XX 26-JUL-1994; 94US-00280864.

XX (AMGE-) AMGEN INC.

XX Eliott SG;

XX WPI; 1996-117004/12.

XX Monoclonal antibodies stimulating an erythropoietin receptor - useful in

XX diagnosis and treatment of patients having disorders associated with low

XX red blood cell levels, e.g. anaemia.

XX Example 6; Page 34; 61pp; English.

XX AAR89960-R89965 and AAR98936-R98939 are overlapping, synthetic human

XX erythropoietin receptor (SHUEPOR) peptides which span residues 1 to 244

XX of the human EPOR. The peptides are used to map the EPOR binding epitope

XX of an EPOR monoclonal antibody which binds to EPORs and stimulates

XX erythropoiesis by stimulating the proliferation and/or differentiation of

XX erythroid progenitor cells to erythrocytes. Pharmaceutical compans.

XX cong. the antibody may be used in the diagnosis and treatment of

XX patients having disorders associated with low red blood cell levels, e.g.

XX anaemia. The antibodies are also useful in methods and kits for detecting

XX EPORs in biological in biological samples

XX Sequence 30 AA;

XX Query Match 100.0%; Score 117; DB 2; Length 30;

XX Best Local Similarity 100.0%; Pred. No. 4.9e-11;

XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX OY 1 QRVETLEGRTCVLSNLRGRTRY 23  
DB 1 QRVETLEGRTCVLSNLRGRTRY 23

## RESULT 5

XX AAB21686  
ID AAB21686 standard; peptide; 211 AA.

XX AAB21686;

XX 21-DEC-2000 (first entry)

DE Human mature erythropoietin receptor EPOR extracellular domain #2.

XX ligand; cell surface receptor; erythropoietin; EPOR; human;

XX protein design automation; FDA.

XX Homo sapiens.

XX WO200047612-A2.

XX 17-AUG-2000.

XX 11-FEB-2000; 2000WO-US003665.

XX 11-FEB-1999; 99US-0120009P.

XX 29-APR-1999; 99US-0131674P.

XX (XENC-) XENCOR INC.

XX Luo P, Dahiyat B;

XX WPI; 2000-549135/50.

XX Screening for ligand analogs and agents which modulate ligand-receptor

XX binding, comprises adding a test ligand to a non-naturally occurring cell

XX surface receptor analog.

XX Example 1; Fig 8; 82pp; English.

XX The present invention relates to a method for screening for a ligand

XX analog, comprising adding a candidate ligand to a non-naturally occurring

XX cell surface receptor analog e.g. erythropoietin receptor (EPOR), and

XX determining the binding of the ligand to the analog. The present sequence

XX is a mature human erythropoietin receptor (EPOR) extracellular domain.

XX Protein Design Automation was carried out on the present sequence, so

XX that it may be used in the present invention as a cell surface receptor

XX analog

XX Sequence 211 AA;

XX Query Match 100.0%; Score 117; DB 3; Length 211;

XX Best Local Similarity 100.0%; Pred. No. 4.7e-10;

XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX OY 1 QRVETLEGRTCVLSNLRGRTRY 23  
DB 161 QRVETLEGRTCVLSNLRGRTRY 163

XX AAB21685  
ID AAB21685 standard; peptide; 225 AA.

XX AAB21685;

XX 21-DEC-2000 (first entry)

XX Human mature erythropoietin receptor EPOR extracellular domain #1.

XX ligand; cell surface receptor; erythropoietin; EPOR; human.

XX Homo sapiens.

XX WO200047612-A2.

XX 17-AUG-2000.

XX 11-FEB-2000; 2000WO-US003665.

XX 11-FEB-1999; 99US-0120009P.

XX 29-APR-1999; 99US-0131674P.

XX (XENC-) XENCOR INC.

PI Luo P, Dahiyat B;  
 XX WPI; 2000-549135/50.  
 XX  
 XX Screening for ligand analogs and agents which modulate ligand-receptor  
 PT binding, comprises adding a test ligand to a non-naturally occurring cell  
 PT surface receptor analog.  
 XX  
 XX Example 1; Fig 8; 82pp; English.  
 XX  
 CC The present invention relates to a method for screening for a ligand  
 CC analog, comprising adding a candidate ligand to a non-naturally occurring  
 CC cell surface receptor analog e.g. erythropoietin receptor (EPOR), and  
 CC determining the binding of the ligand to the analog. The present sequence  
 CC is a mature human erythropoietin receptor (EPOR) extracellular domain.  
 CC This sequence may be used in the present invention as a cell surface  
 CC receptor analog  
 CC  
 XX Sequence 225 AA;  
 SQ  
 Query Match 100.0%; Score 117; DB 3; Length 225;  
 Best Local Similarity 100.0%; Pred. No. 5e-10;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QRVETLEGRTCVLSNLRGRTY 23  
 Db 170 QRVETLEGRTCVLSNLRGRTY 192  
 XX  
 XX RESULT 7  
 XX AAY44622  
 XX ID AAY44622 standard; protein; 438 AA.  
 XX  
 XX AAY44622;  
 XX  
 XX 07-APR-2000 (first entry)  
 XX  
 XX Truncated human EpOR(t439).  
 XX  
 XX Truncated human EpOR; erythropoietin receptor; hypersensitive EpOR(t439);  
 KM mutant human EpOR; EpOR signaling; cancer; infectious disease; HIV;  
 KM sickle cell anaemia; cytostatic; antimicrobial; antiviral;  
 KM immunostimulant; anti-anaemic.  
 XX  
 XX Homo sapiens.  
 XX  
 XX OS  
 XX PN WO9967360-A2.  
 XX  
 XX 29-DEC-1999.  
 XX  
 XX 25-JUN-1999; 99WO-CA000606.  
 XX  
 XX 25-JUN-1998; 98CA-02241576.  
 XX  
 XX 25-JAN-1999; 99CA-02260332.  
 XX  
 XX (HEMO-) HEMOSOL INC.  
 XX  
 XX Bell D, Matthews KE, Mueller SG;  
 XX  
 XX WPI; 2000-136979/12.  
 XX  
 XX P-PSDB; AAZ49634.  
 XX  
 XX Serum free defined medium useful for the efficient culture of stem cells  
 PT used for production of hemoglobin.  
 XX  
 XX Example 6; Fig 9; 61pp; English.  
 XX  
 CC The present sequence is truncated human EpOR (erythropoietin receptor).  
 CC Transfection of constitutively active EpOR(t439) by electroporation into  
 CC a cytokine-dependent cell line supports cell population expansion in the  
 CC absence of exogenous cytokines. Mutant human EpOR is used in treatment of  
 CC disorders related to inadequate EpOR signaling. The transfected cells  
 CC may also used in gene therapy to treat cancer, infectious diseases (e.g.

CC HIV), sickle cell anaemia, and conditions related to abnormal expression  
 CC of erythropoietin  
 XX  
 XX Sequence 438 AA;  
 SQ  
 Query Match 100.0%; Score 117; DB 3; Length 438;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QRVETLEGRTCVLSNLRGRTY 23  
 Db 194 QRVETLEGRTCVLSNLRGRTY 216  
 XX  
 XX RESULT 8  
 XX AAY44623  
 XX ID AAY44623 standard; protein; 438 AA.  
 XX  
 XX AAY44623;  
 XX  
 XX 07-APR-2000 (first entry)  
 XX  
 XX R154C truncated human EpOR(t439).  
 XX  
 XX Truncated human EpOR; erythropoietin receptor; hypersensitive EpOR(t439);  
 KM mutant human EpOR; EpOR signaling; cancer; infectious disease; HIV;  
 KM sickle cell anaemia; cytostatic; antimicrobial; antiviral;  
 KM immunostimulant; anti-anaemic.  
 XX  
 XX Homo sapiens.  
 XX  
 XX OS  
 XX FH Key Location/Qualifiers  
 XX FT Misc-difference 154  
 XX PT /note= "Wild type Arg substituted by Cys"  
 XX  
 XX PN WO9967360-A2.  
 XX  
 XX 29-DEC-1999.  
 XX  
 XX 25-JUN-1999; 99WO-CA000606.  
 XX  
 XX 25-JUN-1998; 98CA-02241576.  
 XX  
 XX 25-JAN-1999; 99CA-02260332.  
 XX  
 XX (HEMO-) HEMOSOL INC.  
 XX  
 XX Bell D, Matthews KE, Mueller SG;  
 XX  
 XX WPI; 2000-136979/12.  
 XX  
 XX N-PSDB; AAZ49636.  
 XX  
 XX Serum free defined medium useful for the efficient culture of stem cells  
 PT used for production of hemoglobin.  
 XX  
 XX Example 6; Fig 10; 61pp; English.  
 XX  
 CC The present sequence is R154C truncated human EpOR (erythropoietin  
 CC receptor). Transfection of constitutively active EpOR(t439; R154C) by  
 CC electroporation into a cytokine-dependent cell line supports cell  
 CC population expansion in the absence of exogenous cytokines. Mutant human  
 CC EpOR is used in treatment of disorders related to inadequate EpOR  
 CC signaling. The transfected cells may also used in gene therapy to treat  
 CC cancer, infectious diseases (e.g. HIV), sickle cell anaemia, and  
 CC conditions related to abnormal expression of erythropoietin  
 CC  
 XX Sequence 438 AA;  
 SQ  
 Query Match 100.0%; Score 117; DB 3; Length 438;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QRVETLEGRTCVLSNLRGRTY 23

| Db       | 194   | QV011EGRTCCVLSNLRGTRY      | 216 |
|----------|---|----------------------------|-----|
| RESULT 9 |   |                            |     |
| AD28671  |   |                            |     |
| ID       | AD28671   | standard; protein; 458 AA. |     |
| XX       |   |                            |     |
| AC       | AD28671;  |                            |     |
| XX       |   |                            |     |
| DT       | 29-JAN-2004   | (first entry)              |     |
| DE       | Human NOV15a protein - SEQ ID 48.                                       |                            |     |
| XX       |   |                            |     |
| KM       | NOVX; antidiabetic; anorectic; cardiact; hypotensive;                   |                            |     |
| KM       | antihypercholesteric; vitruide; antibacterial; fungicide; protozoacide; |                            |     |
| KM       | neurotic; neuroprotective; antiparkinsonian; anticonvulant;             |                            |     |
| KM       | osteopathic; antiarthritic; antiinflammatory; dermatological;           |                            |     |
| KM       | antiallathmic; antilipemic; metabolic; diabetes; obesity; infectious;   |                            |     |
| KM       | anorexia; cancer; cardiovascular; hypertension; atherosclerosis;        |                            |     |
| KM       | neurodegenerative; Alzheimer's disease; Parkinson's; epilepsy; immune;  |                            |     |
| KM       | osteoarthritis; haemopoietic; inflammatory skin; asthma; dyslipidaemia; |                            |     |
| KM       | neurogenesis; cell differentiation; proliferation; haemopoiesis;        |                            |     |
| KM       | wound healing; angiogenesis; gene therapy; chromosome mapping;          |                            |     |
| KM       | tissue typing; human; NOV.  |                            |     |
| XX       |   |                            |     |
| OS       | Homo sapiens.   |                            |     |
| XX       |   |                            |     |
| PN       | MO2003040330-A2.  |                            |     |
| PD       |   |                            |     |
| XX       |   |                            |     |
| PD       | 15-MAY-2003.  |                            |     |
| XX       |   |                            |     |
| PF       |   |                            |     |
| XX       |   |                            |     |
| XX       | 05-NOV-2002; 2002WC-US035536.   |                            |     |
| XX       |   |                            |     |
| PR       | 05-NOV-2001; 2001US-0338626P.   |                            |     |
| PR       | 05-DEC-2001; 2001US-0336600P.   |                            |     |
| PR       | 07-DEC-2001; 2001US-0338285P.   |                            |     |
| PR       | 12-DEC-2001; 2001US-0341346P.   |                            |     |
| PR       | 17-DEC-2001; 2001US-0341477P.   |                            |     |
| PR       | 17-DEC-2001; 2001US-0341540P.   |                            |     |
| PR       | 20-DEC-2001; 2001US-0342592P.   |                            |     |
| PR       | 27-DEC-2001; 2001US-0344287P.   |                            |     |
| PR       | 31-DEC-2001; 2001US-0344903P.   |                            |     |
| PR       | 17-APR-2002; 2002US-0373288P.   |                            |     |
| PR       | 15-MAY-2002; 2002US-0380981P.   |                            |     |
| PR       | 17-MAY-2002; 2002US-0381495P.   |                            |     |
| PR       | 28-MAY-2002; 2002US-0383534P.   |                            |     |
| PR       | 28-MAY-2002; 2002US-0383744P.   |                            |     |
| PR       | 29-MAY-2002; 2002US-0383829P.   |                            |     |
| PR       | 29-MAY-2002; 2002US-0384024P.   |                            |     |
| PR       | 07-AUG-2002; 2002US-0401788P.   |                            |     |
| PR       | 26-AUG-2002; 2002US-0406533P.   |                            |     |
| PR       | 31-OCT-2002; 2002US-00287971.   |                            |     |
| XX       |   |                            |     |
| XX       | (CURA-) CURAGEN CORP.   |                            |     |
| XX       |   |                            |     |
| PI       | Alsbrook JP, Alvarez E, Anderson DW, Baron M, Boldog FL,                |                            |     |
| PI       | Burgess CE, Caeman SJ, Chapoval A, Dhanabal M, Edinger SR, Eisen A,     |                            |     |
| PI       | Ellerman K, Estenberg S, Gangoli EA, Gerlach VL, Gorman L;              |                            |     |
| PI       | Grosse WM, Guo X, Hackett C, Ji W, Kekuda R, Khramtsov NV,              |                            |     |
| PI       | Lepley DW, Li L, Macdonald JF, Mayankar UM, Mazur A, McQueney K;        |                            |     |
| PI       | Meese PS, Miller CE, Millar I, Mishra VS, Padigan M, Patturajan M,      |                            |     |
| PI       | Pena CE, Payman JA, Rastelli L, Rieger DK, Shenoy SG, Shinkets RA;      |                            |     |
| PI       | Smithson G, Sterling G, Spytek KA, Stone DJ, Tchernev VT, Twomlow N     |                            |     |
| PI       | Veneret CM, Zeehuysen BD, Zhong M;                                      |                            |     |
| XX       |   |                            |     |
| DR       | WP1; 2003-441555/41.  |                            |     |
| DR       | N-PSDB; ADE28670.   |                            |     |
| XX       |   |                            |     |
| PT       | New isolated NOVX polypeptides and polynucleotides, useful for          |                            |     |
| PT       | preventing, diagnosing or treating NOVX-associated disorders, e.g.      |                            |     |
| PT       | osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,  |                            |     |
| PT       | asthma, or infections.  |                            |     |
| XX       |   |                            |     |

|           |   |
|-----------|---|
| PS        | Claim 1, SEQ ID NO 48; 447bp; English.                                    |
| XX        |   |
| CC        | The invention relates to a novel isolated NOVX polypeptide. The           |
| CC        | polypeptide of the invention demonstrates, antidiabetic, anorectic,       |
| CC        | cardiant, hypotensive, antiarteriosclerotic, vincidine, antibacterial,    |
| CC        | fungicide, protozoacide, nootropic, neuroprotective, antiparkinsonian,    |
| CC        | anticonvulsant, osteopathic, antirheumatic, antiinflammatory,             |
| CC        | dermatological, antiastrmatic and antilipaeamic activities. The           |
| CC        | polypeptides, nucleic acid molecules and antibodies may be useful for     |
| CC        | treating or diagnosing diseases including metabolic disorders such as     |
| CC        | diabetes and obesity, infectious diseases, anorexia, cancer,              |
| CC        | cardiovascular diseases including hypertension and atherosclerosis,       |
| CC        | neurodegenerative disorders such as Alzheimer's disease, Parkinson's      |
| CC        | disease and epilepsy, immune disorders e.g. osteoarthritis, haemopoietic  |
| CC        | disorders, inflammatory skin disorders, asthma and dyslipidaemia.         |
| CC        | Furthermore, the nucleic acids and polypeptides may also be used to       |
| CC        | identify molecules that modulate or inhibit neurogenesis, cell            |
| CC        | differentiation and proliferation, haemopoiesis, wound healing and        |
| CC        | angiogenesis, as well as in gene therapy. Finally, the nucleic acids may  |
| CC        | be used as hybridisation probes, in chromosome mapping, tissue typing,    |
| CC        | preventive medicine and pharmacogenomics. The current sequence is that of |
| CC        | the human NOVX protein of the invention.                                  |
| XX        |   |
| SQ        | Sequence 458 AA:  |
|           |   |
|           | Query Match 100.0%; Score 117; DB 7; Length 458;                          |
|           | Best Local Similarity 100.0%; Pred. No. 1.1e-09;                          |
|           | Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;               |
| OY        | 1 QRVETLEGRTCECVLSNLGRTRY 23<br>  |
| D6        | 194 QRVETLEGRTCECVLSNLGRTRY 216   |
| RESULT 10 |   |
| ID        | ADE28673 standard; protein: 458 AA.                                       |
| XX        |   |
| AC        | ADE28673;   |
| XX        |   |
| DT        | 29-JAN-2004 (first entry)   |
| XX        |   |
| DE        | Human NOV15b protein - SEQ ID 50.   |
| XX        |   |
| KW        | NOVX; antidiabetic; anorectic; cardiant; hypotensive;                     |
| KW        | antiarteriosclerotic; vincidine; antibacterial; fungicide; protozoacide;  |
| KW        | nootropic; neuroprotective; antiparkinsonian; anticonvulsant;             |
| KW        | osteopathic; antirheumatic; antiinflammatory; dermatological;             |
| KW        | antiastrmatic; antilipaeamic; metabolic; diabetes; obesity; infectious;   |
| KW        | anorexia; cancer; cardiovascular; hypertension; atherosclerosis;          |
| KW        | neurodegenerative; Alzheimer's disease; Parkinson's; epilepsy; immune;    |
| KW        | osteoarthritis; haemopoietic; inflammatory skin; asthma; dyslipidaemia;   |
| KW        | neurogenesis; cell differentiation; proliferation; haemopoiesis;          |
| KW        | wound healing; angiogenesis; gene therapy; chromosome mapping;            |
| KW        | tissue typing; human; NOV.  |
| XX        |   |
| OS        | Homo sapiens.   |
| PW        | WO2003040330-A2.  |
| XX        |   |
| PD        | 15-MAY-2003.  |
| XX        |   |
| PF        | 05-NOV-2002; 2002WO-US035536.   |
| XX        |   |
| PR        | 05-NOV-2001; 2001US-0338626P.   |
| PR        | 05-DEC-2001; 2001US-033600P.  |
| PR        | 07-DEC-2001; 2001US-0338285P.   |
| PR        | 12-DEC-2001; 2001US-0341346P.   |
| PR        | 17-DEC-2001; 2001US-0341477P.   |
| PR        | 17-DEC-2001; 2001US-0341540P.   |
| PR        | 20-DEC-2001; 2001US-0342592P.   |
| PR        | 27-DEC-2001; 2001US-0344297P.   |
| PR        | 31-DEC-2001; 2001US-0344903P.   |





```

Db          194 QRVETLGRTECVLSNLGRTRY 216

RESULT 14
ID AAR06512 standard; protein; 508 AA.
XX
AC AAR06512;
XX
DT 25-MAR-2003 (revised)
DT 04-JAN-1991 (first entry)
XX
DE EPO receptor.
XX
KM Erythropoietin; Diamond Blackfan anaemia; polycythemia vera.
XX
OS Homo sapiens.
XX
PN W09008822-A.
XX
PD 09-AUG-1990.
XX
PF 03-FEB-1989; 89US-00306503.
XX
PR 03-FEB-1989; 89US-00306503.
XX
PA (GEMV ) GENETICS INST INC.
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI Dandrea A, Wong G;
XX
DR WPI; 1990-260931/34.
DR N-PSDB; AAQ05748.
XX
PT Erythropoietin receptor and gene - used for developing reagents and
PT systems to control and study erythropoiesis.
XX
PS Disclosure; Fig 2; 53pp; English.
XX
CC The sequence was deduced from DNA obt'd. from a clone isolated from a
CC commercially available human genomic cDNA library in phage Lambda Fix
CC (Stratagene). The sequence encodes a type I trans- membrane protein with
CC binding affinity for EPO. The gene and recombinant EPO receptor produced
CC on expression of the DNA are used to develop reagents and systems to
CC control and study erythropoiesis. It is believed that the EPO receptor is
CC dys- functional in individuals with Diamond Blackfan anaemia, and may be
CC hyperactive in polycythemia vera. See also AAR06511 (murine EPO
CC receptor). (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-
CC MAR-2003 to correct PI field.)
XX
SQ Sequence 508 AA;

Query Match          100.0%; Score 117; DB 2; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 QRVETLGRTECVLSNLGRTRY 23
Db          194 QRVETLGRTECVLSNLGRTRY 216

```

```

XX          XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Peptide 1..24 /note="signal peptide"
FT Protein 25..508 /note="mature EPO receptor"
FT Region 251..272 /note="putative transmembrane domain"
XX
XX
PN US5278065-A.
XX
PD 11-JAN-1994.
XX
PF 25-MAR-1991; 91US-00678877.
XX
PR 03-FEB-1989; 89US-00306503.
XX
PA (GEMV ) GENETICS INST INC.
PA (CHIL-) CHILDRENS MEDICAL CENT.
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI D'andrea A, Wong GG, Jones SS;
XX
DR WPI; 1994-025409/03.
DR N-PSDB; AAQ53995.
XX
PT Recombinant DNA encoding erythropoietin receptor - used to develop prods.
PT for study, treatment or diagnosis of disorders in which receptor is
PT dysfunctional.
XX
PS Disclosure; Fig 9; 24pp; English.
XX
CC Mouse erythroleukemia (HEL) cells were used to construct a cDNA library.
CC The cDNA was used to transfect COS-1 cells and these were screened for
CC radioliodinated erythropoietin (EPO) binding to isolate cDNA encoding the
CC EPO receptor. This cDNA was used as a probe to screen a human genomic
CC cDNA library to obtain DNA encoding the human EPO receptor. The cDNA may
CC be used to study, treat or diagnose disorders in which the EPO receptor
CC is dysfunctional. The EPO receptor may also be used to raise antibodies or
CC for treating hypersensitivity to EPO or who have elevated levels of EPO.
CC The pord. is pref. used for treating anaemias, primary proliferative
CC polycythemia and secondary polycythemia. See also AAR47517. (Updated on
CC 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 508 AA;

Query Match          100.0%; Score 117; DB 2; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 QRVETLGRTECVLSNLGRTRY 23
Db          194 QRVETLGRTECVLSNLGRTRY 216

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Search completed: May 6, 2004, 12:45:02  
Job time : 55 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 6, 2004, 12:42:22 ; Search time 23 Seconds  
(without alignments)  
51.626 Million cell updates/sec

Title: US-10-612-885A-1  
Perfect score: 117  
Sequence: 1 QWEILLEGRETCVLSNLRGRTRY 23

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues  
Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep.\*  
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4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID                   | Description       |
|------------|-------|-------------|--------|----------------------|-------------------|
| 1          | 117   | 100.0       | 23     | US-09-028-937-11     | Sequence 11, Appl |
| 2          | 117   | 100.0       | 30     | US-08-280-864A-12    | Sequence 12, Appl |
| 3          | 117   | 100.0       | 30     | US-09-092-291-12     | Sequence 12, Appl |
| 4          | 117   | 100.0       | 438    | US-09-339-838-5      | Sequence 5, Appl  |
| 5          | 117   | 100.0       | 438    | US-09-339-838-7      | Sequence 7, Appl  |
| 6          | 117   | 100.0       | 488    | US-08-736-511-2      | Sequence 2, Appl  |
| 7          | 117   | 100.0       | 508    | US-08-850-293-5      | Sequence 5, Appl  |
| 8          | 49    | 41.9        | 321    | US-09-039-609-4      | Sequence 4, Appl  |
| 9          | 49    | 41.9        | 458    | US-09-039-609-2      | Sequence 2, Appl  |
| 10         | 46    | 39.3        | 64     | US-09-134-000C-5287  | Sequence 5287, Ap |
| 11         | 46    | 39.3        | 67     | US-09-732-210-1599   | Sequence 1599, Ap |
| 12         | 46    | 39.3        | 67     | US-09-732-210-1600   | Sequence 1600, Ap |
| 13         | 45    | 38.5        | 372    | US-09-252-991A-32067 | Sequence 32067, A |
| 14         | 44    | 37.6        | 493    | US-09-489-039A-12903 | Sequence 12903, A |
| 15         | 43    | 36.8        | 931    | US-08-624-655A-2     | Sequence 2, Appl  |
| 16         | 42    | 35.9        | 67     | US-09-732-210-1601   | Sequence 1601, Ap |
| 17         | 42    | 35.9        | 252    | US-09-252-991A-32222 | Sequence 32222, A |
| 18         | 42    | 35.9        | 283    | US-08-956-171E-5203  | Sequence 5203, Ap |
| 19         | 42    | 35.9        | 363    | US-09-134-000C-3764  | Sequence 3764, Ap |
| 20         | 42    | 35.9        | 605    | US-08-752-307B-8     | Sequence 8, Appl  |
| 21         | 42    | 35.9        | 605    | US-09-707-802-8      | Sequence 8, Appl  |
| 22         | 42    | 35.9        | 605    | US-09-991-326-8      | Sequence 8, Appl  |
| 23         | 42    | 35.9        | 623    | US-09-252-991A-23930 | Sequence 23930, A |
| 24         | 42    | 35.9        | 1018   | US-08-452-052-2      | Sequence 2, Appl  |
| 25         | 42    | 35.9        | 1101   | US-08-986-485-2      | Sequence 2, Appl  |
| 26         | 42    | 35.9        | 1611   | US-08-804-227C-5     | Sequence 5, Appl  |
| 27         | 42    | 35.9        | 3729   | US-08-804-227C-4     | Sequence 4, Appl  |

|    |    |      |      |   |                      |                    |
|----|----|------|------|---|----------------------|--------------------|
| 28 | 42 | 35.9 | 4472 | 2 | US-08-804-227C-2     | Sequence 2, Appl   |
| 29 | 42 | 35.9 | 4545 | 2 | US-08-804-227C-14    | Sequence 14, Appl  |
| 30 | 41 | 35.0 | 50   | 4 | US-09-621-976-6212   | Sequence 6212, Ap  |
| 31 | 41 | 35.0 | 60   | 4 | US-08-754-477A-14    | Sequence 14, Appl  |
| 32 | 41 | 35.0 | 60   | 4 | US-08-754-477A-15    | Sequence 15, Appl  |
| 33 | 41 | 35.0 | 75   | 3 | US-08-928-383B-13    | Sequence 438, Appl |
| 34 | 41 | 35.0 | 292  | 4 | US-09-711-164-438    | Sequence 438, Appl |
| 35 | 41 | 35.0 | 337  | 4 | US-09-134-001C-3535  | Sequence 3535, Ap  |
| 36 | 41 | 35.0 | 749  | 4 | US-09-252-991A-17331 | Sequence 17331, A  |
| 37 | 41 | 35.0 | 835  | 4 | US-09-758-282B-155   | Sequence 155, App  |
| 38 | 41 | 35.0 | 835  | 4 | US-09-758-282B-243   | Sequence 243, App  |
| 39 | 41 | 35.0 | 843  | 4 | US-09-489-039A-7545  | Sequence 7545, Ap  |
| 40 | 41 | 35.0 | 865  | 4 | US-09-252-991A-20894 | Sequence 20894, A  |
| 41 | 41 | 35.0 | 1018 | 1 | US-08-408-093-6      | Sequence 6, Appl   |
| 42 | 41 | 35.0 | 1018 | 1 | US-08-408-420A-6     | Sequence 6, Appl   |
| 43 | 41 | 35.0 | 1018 | 1 | US-08-714-901-6      | Sequence 6, Appl   |
| 44 | 41 | 35.0 | 1018 | 3 | US-08-040-741-6      | Sequence 6, Appl   |
| 45 | 41 | 35.0 | 1091 | 3 | US-08-986-485-5      | Sequence 5, Appl   |

## ALIGNMENTS

RESULT 1  
US-09-028-937-11  
Sequence 11, Application US/09028937  
Patent No. 633031  
GENERAL INFORMATION:  
APPLICANT: Olsson, Lennart  
APPLICANT: Naranda, Tatjana  
TITLE OF INVENTION: Receptor Derived Peptides As Modulators  
TITLE OF INVENTION: Of Receptor Activity  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Flehr, Hohbach, Teest, Albritton & Herbert  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/028,937  
CLASSIFICATION:  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/788,820  
FILING DATE: 23-JAN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/701,382  
FILING DATE: 22-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/612,999  
FILING DATE: 08-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Silva, Robin M.  
REGISTRATION NUMBER: 38,304  
REFERENCE/DOCKET NUMBER: A-63139-3/RFT/RMS  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 949-8711  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-09-028-937-11

Query Match 100.0%; Score 117; DB 4; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.3e-12;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRVLEIGRTECVLSNLRGRTRY 23  
Db 1 QRVLEIGRTECVLSNLRGRTRY 23

RESULT 2  
US-08-280-864A-12

; Sequence 12, Application US/08280864A  
; Patent No. 5885574  
; GENERAL INFORMATION:  
; APPLICANT: Eliott, Steven G.  
; TITLE OF INVENTION: Antibodies Which Activate an  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Denavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 91320  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/280,864A  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-307  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 30 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-280-864A-12

Query Match 100.0%; Score 117; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.8e-12;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRVLEIGRTECVLSNLRGRTRY 23  
Db 1 QRVLEIGRTECVLSNLRGRTRY 23

RESULT 3  
US-09-092-291-12

; Sequence 12, Application US/09092291  
; Patent No. 6319499  
; GENERAL INFORMATION:  
; APPLICANT: Eliott, Steven G.  
; TITLE OF INVENTION: Antibodies Which Activate an  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: One Amgen Center Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 91320  
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/092,291  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION NUMBER:  
; APPLICATION NUMBER: US 08/280864  
; FILING DATE: 25-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-307A  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 30 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-092-291-12

Query Match 100.0%; Score 117; DB 4; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.8e-12;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRVLEIGRTECVLSNLRGRTRY 23  
Db 1 QRVLEIGRTECVLSNLRGRTRY 23

RESULT 4  
US-09-339-838-5

; Sequence 5, Application US/09339838  
; Patent No. 6361998  
; GENERAL INFORMATION:  
; APPLICANT: Bell, David N.  
; APPLICANT: Mueller, Susan G.  
; APPLICANT: Matthews, Kathryn E.  
; TITLE OF INVENTION: The Efficient Culture of Stem Cells for the Production of Hemoglot  
; FILE REFERENCE: 6704-83  
; CURRENT APPLICATION NUMBER: US/09/339,838  
; CURRENT FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: CA 2,260,332  
; PRIOR FILING DATE: 1999-01-25  
; PRIOR APPLICATION NUMBER: CA 2,241,576  
; PRIOR FILING DATE: 1998-06-25  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 5  
; LENGTH: 438  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-339-838-5

Query Match 100.0%; Score 117; DB 4; Length 438;  
Best Local Similarity 100.0%; Pred. No. 4.3e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRVLEIGRTECVLSNLRGRTRY 23  
Db 194 QRVLEIGRTECVLSNLRGRTRY 216

RESULT 5  
US-09-339-838-7

; Sequence 7, Application US/09339838  
; Patent No. 6361998  
; GENERAL INFORMATION:  
; APPLICANT: Bell, David N.  
; APPLICANT: Mueller, Susan G.  
; APPLICANT: Matthews, Kathryn E.



TITLE OF INVENTION: The Efficient Culture of Stem Cells for the Production of Hemogid  
FILE REFERENCE: 6704-83  
CURRENT APPLICATION NUMBER: US/09/339,838  
CURRENT FILING DATE: 1999-06-25  
PRIOR APPLICATION NUMBER: CA 2,260,332  
PRIOR FILING DATE: 1999-01-25  
PRIOR APPLICATION NUMBER: CA 2,241,576  
PRIOR FILING DATE: 1998-06-25  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 7  
LENGTH: 438  
TYPE: PR  
ORGANISM: Homo sapiens  
US-09-339-838-7

Query Match 100.0%; Score 117; DB 4; Length 438;  
Best Local Similarity 100.0%; Pred. No. 4.3e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ORVEILGRTCVLSNLRGTRY 23  
DB 194 ORVEILGRTCVLSNLRGTRY 216

RESULT 6  
US-08-776-511-2  
Sequence 2, Application US/0876511  
Patent No. 6153190  
GENERAL INFORMATION:  
APPLICANT: Young, Peter R.  
ATTORNEY/AGENT INFORMATION:  
TITLE OF INVENTION: Method for Obtaining Receptor Agonist  
TITLE OF INVENTION: Antibodies  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation- Corporate  
ADDRESS: Patents  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19406-2799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/776,511  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Jervis, Herbert H.  
REGISTRATION NUMBER: 31,171  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5015  
TELEFAX: 610-270-5090  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 488 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-776-511-2

Query Match 100.0%; Score 117; DB 3; Length 488;  
Best Local Similarity 100.0%; Pred. No. 4.9e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ORVEILGRTCVLSNLRGTRY 23  
DB 194 ORVEILGRTCVLSNLRGTRY 216

DB 194 ORVEILGRTCVLSNLRGTRY 216

RESULT 7  
US-08-850-293-5  
Sequence 5, Application US/08850293  
Patent No. 5843726  
GENERAL INFORMATION:  
APPLICANT: Lee, Jong Y.  
TITLE OF INVENTION: PURIFIED HUMAN ERYTHROPOIETIN RECEPTOR  
TITLE OF INVENTION: PROTEIN FRAGMENT AND ANTIBODIES DERIVED THEREFROM  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C., P.A.  
STREET: 60 South Sixth Street, Suite 3300  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/850,293  
FILING DATE: 05-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/499,643  
FILING DATE: 07-JUL-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/106,815  
FILING DATE: 16-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Ellinger, Mark S.  
REGISTRATION NUMBER: 34,812  
REFERENCE/DOCKET NUMBER: 07004/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612/335-5070  
TELEFAX: 612/288-9696  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 508 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-850-293-5

Query Match 100.0%; Score 117; DB 2; Length 508;  
Best Local Similarity 100.0%; Pred. No. 5.2e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ORVEILGRTCVLSNLRGTRY 23  
DB 194 ORVEILGRTCVLSNLRGTRY 216

RESULT 8  
US-09-039-609-4  
Sequence 4, Application US/09039609  
Patent No. 6107473  
GENERAL INFORMATION:  
APPLICANT: ALBONE, EARL  
ATTORNEY/AGENT INFORMATION:  
TITLE OF INVENTION: A KRINGLE-RELATED CLONE,  
TITLE OF INVENTION: HTHE247  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ratner & Prestia  
STREET: P.O. Box 980  
CITY: Valley Forge  
STATE: PA

COUNTRY: USA  
ZIP: 19482  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/039,609  
FILING DATE: 16-MAR-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/060,623  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Prestia, Paul F  
REGISTRATION NUMBER: 23,031  
REFERENCE/DOCKET NUMBER: GP-70275  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-407-0700  
TELEFAX: 610-407-0701  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 321 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-039-609-4

Query Match 41.9%; Score 49; DB 3; Length 321;  
Best Local Similarity 50.0%; Pred. No. 4.1;  
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
QY 3 VELIEGTECVLSNLGRTR 22  
DB 226 VELLDGYTHVLARFGRSR 245

RESULT 9  
US-09-039-609-2  
Sequence 2, Application US/09039609  
Patent No. 6107473  
GENERAL INFORMATION:  
APPLICANT: ALBONE, EARL  
APPLICANT: KIKLY, KRISTINE  
TITLE OF INVENTION: A KIRINLE-RELATED CLONE,  
TITLE OF INVENTION: HTHB247  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ratner & Prestia  
STREET: P.O. Box 980  
CITY: Valley Forge  
STATE: PA  
COUNTRY: USA  
ZIP: 19482  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/039,609  
FILING DATE: 16-MAR-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/060,623  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Prestia, Paul F  
REGISTRATION NUMBER: 23,031  
REFERENCE/DOCKET NUMBER: GP-70275

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-407-0700  
TELEFAX: 610-407-0701  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 458 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-039-609-2

Query Match 41.9%; Score 49; DB 3; Length 458;  
Best Local Similarity 50.0%; Pred. No. 6.3;  
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
QY 3 VELIEGTECVLSNLGRTR 22  
DB 270 VELLDGYTHVLARFGRSR 289

RESULT 10  
US-09-134-000C-5287  
Sequence 5287, Application US/09134000C  
Patent No. 6617156  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
FILE REFERENCE: 032796-032  
CURRENT APPLICATION NUMBER: US/09/134,000C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/055,778  
PRIOR FILING DATE: 1997-08-15  
NUMBER OF SEQ ID NOS: 6812  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 5287  
LENGTH: 64  
TYPE: PRT  
ORGANISM: Enterococcus faecalis  
US-09-134-000C-5287

Query Match 39.3%; Score 46; DB 4; Length 64;  
Best Local Similarity 60.0%; Pred. No. 1.9;  
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 VELIEGTECVLSNL 17  
DB 11 VELIEGTEGTERQLTNM 25

RESULT 11  
US-09-732-210-1599  
Sequence 1599, Application US/09732210  
Patent No. 6573361  
GENERAL INFORMATION:  
APPLICANT: Bunkers, Greg J.  
APPLICANT: Liang, Jihong  
APPLICANT: Miltenek, Cindy A.  
APPLICANT: Seale, Jeffrey W.  
APPLICANT: Wu, Yonnie S.  
TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use  
FILE REFERENCE: 38-21(15036)B  
CURRENT APPLICATION NUMBER: US/09/732,210  
CURRENT FILING DATE: 2000-12-07  
PRIOR APPLICATION NUMBER: US 60/169,513  
PRIOR FILING DATE: 1999-12-07  
PRIOR APPLICATION NUMBER: US 60/169,340  
PRIOR FILING DATE: 1999-12-07  
NUMBER OF SEQ ID NOS: 1753  
SEQ ID NO 1599  
LENGTH: 67

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/ TYPE: PRT
/ ORGANISM: Kluyveromyces lactis
US-09-732-210-1599

Query Match      39.3%; Score 46; DB 4; Length 67;
Best Local Similarity 42.9%; Pred. No. 2;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY      2 RVELEGRTECVLSNLGRTR 22
Db      29 RVEFLEDTTRTIVNVKGPVR 49

RESULT 12
US-09-732-210-1600
/ Sequence 1600, Application US/09732210
/ Patent No. 6573361
/ GENERAL INFORMATION:
/ APPLICANT: Bunkers, Greg J.
/ APPLICANT: Miltanck, Cindy A.
/ APPLICANT: Seale, Jeffrey W.
/ APPLICANT: Wu, Yonnie S.
/ TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
/ FILE REFERENCE: 38-21(15036)B
/ CURRENT APPLICATION NUMBER: US/09/732,210
/ CURRENT FILING DATE: 2000-12-07
/ PRIOR APPLICATION NUMBER: US 60/169,513
/ PRIOR FILING DATE: 1999-12-07
/ PRIOR APPLICATION NUMBER: US 60/169,340
/ PRIOR FILING DATE: 1999-12-07
/ NUMBER OF SEQ ID NOS: 1753
/ SEQ ID NO 1600
/ LENGTH: 67
/ TYPE: PRT
/ ORGANISM: Kluyveromyces marxianus
US-09-732-210-1600

Query Match      39.3%; Score 46; DB 4; Length 67;
Best Local Similarity 42.9%; Pred. No. 2;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY      2 RVELEGRTECVLSNLGRTR 22
Db      29 RVEFLEDTTRTIVNVKGPVR 49

RESULT 13
US-09-252-991A-32067
/ Sequence 32067, Application US/09252991A
/ Patent No. 6551795
/ GENERAL INFORMATION:
/ APPLICANT: Marc J. Rubenfield et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/ TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 107196.136
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ CURRENT FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/074,788
/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/094,190
/ PRIOR FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 31142
/ SEQ ID NO 32067
/ LENGTH: 372
/ TYPE: PRT
/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32067

Query Match      38.5%; Score 45; DB 4; Length 372;
Best Local Similarity 54.5%; Pred. No. 22;
Matches 12; Conservative 2; Mismatches 6; Indels 2; Gaps 1;
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QY      2 RVELEGRTECVLSNLGRTRY 23
Db      251 RVAVLGRVE--LSPLHGRGM 270

RESULT 14
US-09-489-039A-12903
/ Sequence 12903, Application US/09489039A
/ Patent No. 6610836
/ GENERAL INFORMATION:
/ APPLICANT: Gary Breton et. al
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
/ TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 2709.2004001
/ CURRENT APPLICATION NUMBER: US/09/489,039A
/ CURRENT FILING DATE: 2000-01-27
/ PRIOR APPLICATION NUMBER: US 60/117,747
/ PRIOR FILING DATE: 1999-01-29
/ NUMBER OF SEQ ID NOS: 14342
/ SEQ ID NO 12903
/ LENGTH: 493
/ TYPE: PRT
/ ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12903

Query Match      37.6%; Score 44; DB 4; Length 493;
Best Local Similarity 45.0%; Pred. No. 45;
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY      4 ELEGRTECVLSNLGRTRY 23
Db      111 EALEGKTFCVVRKRGKHEP 130

RESULT 15
US-08-624-655A-2
/ Sequence 2, Application US/08624655A
/ Patent No. 6323005
/ GENERAL INFORMATION:
/ APPLICANT: DABAN, MONTSERRAT
/ APPLICANT: MEDRANO, ANDRES
/ APPLICANT: ESPUNA, ENRIC
/ APPLICANT: QUEROLO, ENRIQUE
/ TITLE OF INVENTION: TRANSFERRIN-BINDING PROTEIN 1 (Tbp1) GENE OF
/ TITLE OF INVENTION: Actinobacillus pleuropneumoniae, ITS USE TO PREPARE
/ TITLE OF INVENTION: PRODUCTS FOR THE UTILIZATION IN VACCINES FOR
/ TITLE OF INVENTION: PLEURO-PNEUMONIA AND AS DIAGNOSTIC REAGENTS
/ FILE REFERENCE: P00740
/ CURRENT APPLICATION NUMBER: US/08/624,655A
/ CURRENT FILING DATE: 1996-03-22
/ PRIOR APPLICATION NUMBER: 95 00592
/ PRIOR FILING DATE: 1995-03-24
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 931
/ TYPE: PRT
/ ORGANISM: Actinobacillus pleuropneumoniae
US-08-624-655A-2

Query Match      36.8%; Score 43; DB 4; Length 931;
Best Local Similarity 33.3%; Pred. No. 1.4e+02;
Matches 6; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY      6 LEGRTECVLSNLGRTRY 23
Db      581 IAGRADCATSKIKGHNHV 598

Search completed: May 6, 2004, 12:46:53
Job time : 23 secs
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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: May 6, 2004, 12:45:07 ; Search time 42 Seconds  
(Without alignments)  
152.001 Million cell updates/sec

Title: US-10-612-885A-1

Perfect score: 117  
Sequence: 1 QRVETLEGRTECVLSNLRGRTRY 23Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1140673 seqs, 27566755 residues

Total number of hits satisfying chosen parameters: 1140673

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID                | Description       |
|------------|-------|-------------|--------|----------------------|-------------------|
| 1          | 117   | 100.0       | 23     | 9 US-09-991-548-11   | Sequence 11, Appl |
| 2          | 117   | 100.0       | 23     | 16 US-10-231-494-30  | Sequence 10, Appl |
| 3          | 117   | 100.0       | 30     | 15 US-10-364-276-12  | Sequence 12, Appl |
| 4          | 117   | 100.0       | 458    | 12 US-10-287-871-48  | Sequence 48, Appl |
| 5          | 117   | 100.0       | 458    | 12 US-10-287-871-50  | Sequence 50, Appl |
| 6          | 117   | 100.0       | 458    | 12 US-10-287-871-52  | Sequence 52, Appl |
| 7          | 117   | 100.0       | 508    | 9 US-09-016-159-5    | Sequence 5, Appl  |
| 8          | 113   | 96.6        | 508    | 12 US-10-287-871-54  | Sequence 54, Appl |
| 9          | 103   | 88.0        | 109    | 15 US-10-316-194-142 | Sequence 142, App |
| 10         | 96    | 82.1        | 109    | 15 US-10-316-194-144 | Sequence 144, App |
| 11         | 93    | 79.5        | 109    | 15 US-10-316-194-35  | Sequence 35, Appl |
| 12         | 86    | 73.5        | 109    | 15 US-10-316-194-43  | Sequence 43, Appl |
| 13         | 52    | 44.4        | 1026   | 10 US-09-947-063-4   | Sequence 4, Appl  |
| 14         | 52    | 44.4        | 1026   | 10 US-09-947-063-11  | Sequence 11, Appl |
| 15         | 49    | 41.9        | 49     | 9 US-09-728-912-7    | Sequence 7, Appl  |

|    |      |      |     |                         |                   |
|----|------|------|-----|-------------------------|-------------------|
| 16 | 49   | 41.9 | 110 | 14 US-10-029-386-27439  | Sequence 27439, A |
| 17 | 49   | 41.9 | 341 | 9 US-09-848-288-4       | Sequence 4, Appl  |
| 18 | 49   | 41.9 | 373 | 10 US-09-759-130B-376   | Sequence 376, App |
| 19 | 49   | 41.9 | 373 | 13 US-10-042-431-6      | Sequence 6, Appl  |
| 20 | 49   | 41.9 | 413 | 9 US-09-728-912-2       | Sequence 2, Appl  |
| 21 | 49   | 41.9 | 451 | 10 US-09-759-130B-413   | Sequence 413, App |
| 22 | 49   | 41.9 | 451 | 13 US-10-042-431-43     | Sequence 43, Appl |
| 23 | 49   | 41.9 | 456 | 10 US-09-759-130B-375   | Sequence 375, App |
| 24 | 49   | 41.9 | 456 | 13 US-10-042-431-5      | Sequence 5, Appl  |
| 25 | 49   | 41.9 | 458 | 16 US-10-467-042-16     | Sequence 16, Appl |
| 26 | 49   | 41.9 | 470 | 10 US-09-759-130B-439   | Sequence 439, App |
| 27 | 49   | 41.9 | 470 | 13 US-10-042-431-69     | Sequence 69, Appl |
| 28 | 49   | 41.9 | 475 | 10 US-09-759-130B-373   | Sequence 373, App |
| 29 | 49   | 41.9 | 475 | 13 US-10-042-431-3      | Sequence 3, Appl  |
| 30 | 49   | 41.9 | 482 | 15 US-10-094-749-2546   | Sequence 2546, Ap |
| 31 | 48   | 41.0 | 312 | 9 US-09-738-626-5282    | Sequence 5282, Ap |
| 32 | 47.5 | 40.6 | 419 | 15 US-10-369-493-9725   | Sequence 9725, Ap |
| 33 | 47   | 40.2 | 85  | 14 US-10-029-386-32900  | Sequence 32900, A |
| 34 | 47   | 40.2 | 151 | 12 US-10-424-599-181458 | Sequence 181458,  |
| 35 | 47   | 40.2 | 386 | 12 US-10-424-599-181457 | Sequence 181457,  |
| 36 | 46   | 39.3 | 494 | 12 US-10-425-114-50005  | Sequence 50005, A |
| 37 | 46   | 39.3 | 941 | 12 US-10-425-114-72012  | Sequence 72012, A |
| 38 | 45   | 38.5 | 686 | 15 US-10-162-335-46     | Sequence 46, Appl |
| 39 | 45   | 38.5 | 686 | 15 US-10-162-335-48     | Sequence 48, Appl |
| 40 | 45   | 38.5 | 686 | 15 US-10-162-335-50     | Sequence 50, Appl |
| 41 | 45   | 38.5 | 686 | 15 US-10-162-335-52     | Sequence 52, Appl |
| 42 | 45   | 38.5 | 961 | 15 US-10-162-335-42     | Sequence 42, Appl |
| 43 | 44   | 37.6 | 87  | 12 US-10-424-599-196538 | Sequence 196538,  |
| 44 | 44   | 37.6 | 250 | 12 US-10-424-599-236053 | Sequence 236053,  |
| 45 | 44   | 37.6 | 873 | 12 US-10-425-114-65968  | Sequence 65968, A |

## ALIGNMENTS

```
RESULT 1
US-09-991-548-11
Sequence 11, Application US/09991548
Patent No. US20020160013A1
GENERAL INFORMATION:
APPLICANT: OLSSON, Lennart
TITLE OF INVENTION: RECEPTOR DERIVED PEPTIDES AS MODULATORS
TITLE OF INVENTION: OF RECEPTOR ACTIVITY
FILE REFERENCE: 213542000101
CURRENT APPLICATION NUMBER: US/09/991,548
PRIOR FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 09/028,937
PRIOR FILING DATE: 1998-02-24
PRIOR APPLICATION NUMBER: 08/788,820
PRIOR FILING DATE: 1997-01-23
PRIOR APPLICATION NUMBER: 08/701,382
PRIOR FILING DATE: 1996-08-22
PRIOR APPLICATION NUMBER: 08/612,999
PRIOR FILING DATE: 1996-03-08
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 23
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: human erythropoietin receptor
US-09-991-548-11
```

Query Match 100.0%; Score 117; DB 9; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.8e-11;  
Matches 23; Conservativity 0; Mismatches 0; Indels 0;  
Gaps 0;

QY 1 QRVETLEGRTECVLSNLRGRTRY 23  
DB 1 QRVETLEGRTECVLSNLRGRTRY 23

RESULT 2  
US-10-231-494-30  
; Sequence 30, Application US/10231494  
; Publication No. US2004002334A1  
; GENERAL INFORMATION:  
; APPLICANT: Prior, Christopher P.  
; TITLE OF INVENTION: Modified Transferrin Fusion Proteins  
; FILE REFERENCE: 54710-5001-US  
; CURRENT APPLICATION NUMBER: US/10/231,494  
; CURRENT FILING DATE: 2002-08-30  
; PRIOR APPLICATION NUMBER: US 60/315,745  
; PRIOR FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: US 60/334,059  
; PRIOR FILING DATE: 2001-11-30  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: Patentn Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 23  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; OTHER INFORMATION: Description of Artificial Sequence: EPO mimetic  
; OTHER INFORMATION: peptide  
US-10-231-494-30

Query Match 100.0%; Score 117; DB 16; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.8e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRVLEIGRTECVLSNLRGRTRY 23  
Db 1 QRVLEIGRTECVLSNLRGRTRY 23

RESULT 3  
US-10-364-276-12  
; Sequence 12, Application US/10364276  
; Publication No. US2003021544A1  
; GENERAL INFORMATION:  
; APPLICANT: Elliott, Steven G  
; TITLE OF INVENTION: Antibodies which Activate an Erythropoietin Receptor  
; FILE REFERENCE: 06843-0030-04000  
; CURRENT APPLICATION NUMBER: US/10/364,276  
; CURRENT FILING DATE: 2003-06-17  
; PRIOR APPLICATION NUMBER: 09/092,671  
; PRIOR FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 08/280,864  
; PRIOR FILING DATE: 1994-07-26  
; PRIOR APPLICATION NUMBER: 09/640,090  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patentn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 30  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-10-364-276-12

Query Match 100.0%; Score 117; DB 15; Length 30;  
Best Local Similarity 100.0%; Pred. No. 2.5e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRVLEIGRTECVLSNLRGRTRY 23  
Db 1 QRVLEIGRTECVLSNLRGRTRY 23

RESULT 4  
US-10-287-971-48

; Sequence 48, Application US/10287971  
; Publication No. US20040067882A1  
; GENERAL INFORMATION:  
; APPLICANT: Alsobrook, et al  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS  
; FILE REFERENCE: 21402-480A  
; CURRENT APPLICATION NUMBER: US/10/287,971  
; CURRENT FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: 09/997,425  
; PRIOR FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: 10/035,568  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: 60/338,626  
; PRIOR FILING DATE: 2001-11-05  
; PRIOR APPLICATION NUMBER: 60/401,479  
; PRIOR FILING DATE: 2002-08-06  
; PRIOR APPLICATION NUMBER: 60/333,072  
; PRIOR FILING DATE: 2001-11-06  
; PRIOR APPLICATION NUMBER: 60/348,283  
; PRIOR FILING DATE: 2001-11-09  
; PRIOR APPLICATION NUMBER: 60/393,262  
; PRIOR FILING DATE: 2002-07-02  
; PRIOR APPLICATION NUMBER: 60/406,181  
; PRIOR FILING DATE: 2002-08-26  
; NUMBER OF SEQ ID NOS: 397  
; SOFTWARE: CuraSeqList version 0.1  
; SEQ ID NO 48  
; LENGTH: 458  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-287-971-48

Query Match 100.0%; Score 117; DB 12; Length 458;  
Best Local Similarity 100.0%; Pred. No. 5.6e-10;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRVLEIGRTECVLSNLRGRTRY 23  
Db 194 QRVLEIGRTECVLSNLRGRTRY 216

RESULT 5  
US-10-287-971-50  
; Sequence 50, Application US/10287971  
; Publication No. US20040067882A1  
; GENERAL INFORMATION:  
; APPLICANT: Alsobrook, et al  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS  
; FILE REFERENCE: 21402-480A  
; CURRENT APPLICATION NUMBER: US/10/287,971  
; CURRENT FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: 09/997,425  
; PRIOR FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: 10/035,568  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: 60/338,626  
; PRIOR FILING DATE: 2001-11-05  
; PRIOR APPLICATION NUMBER: 60/401,479  
; PRIOR FILING DATE: 2002-08-06  
; PRIOR APPLICATION NUMBER: 60/333,072  
; PRIOR FILING DATE: 2001-11-06  
; PRIOR APPLICATION NUMBER: 60/348,283  
; PRIOR FILING DATE: 2001-11-09  
; PRIOR APPLICATION NUMBER: 60/393,262  
; PRIOR FILING DATE: 2002-07-02  
; PRIOR APPLICATION NUMBER: 60/406,181  
; PRIOR FILING DATE: 2002-08-26  
; NUMBER OF SEQ ID NOS: 397  
; SOFTWARE: CuraSeqList version 0.1  
; SEQ ID NO 50  
; LENGTH: 458  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-10-287-971-50

Query Match 100.0%; Score 117; DB 12; Length 458;  
Best Local Similarity 100.0%; Pred. No. 5.6e-10;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ORVEILEGRTECVLSNLRGRTRY 23  
|||  
Db 194 ORVEILEGRTECVLSNLRGRTRY 216

RESULT 6

US-10-287-971-52  
; Sequence 52, Application US/10287971  
; Publication No. US20040067882A1  
; GENERAL INFORMATION:  
; APPLICANT: Alcobrook, et al  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-480A  
; CURRENT APPLICATION NUMBER: US/10/287,971  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: 09/997,425  
; PRIOR FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: 10/035,568  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: 60/338,626  
; PRIOR FILING DATE: 2001-11-05  
; PRIOR APPLICATION NUMBER: 60/401,479  
; PRIOR FILING DATE: 2002-08-06  
; PRIOR APPLICATION NUMBER: 60/333,072  
; PRIOR FILING DATE: 2001-11-06  
; PRIOR APPLICATION NUMBER: 60/348,283  
; PRIOR FILING DATE: 2001-11-09  
; PRIOR APPLICATION NUMBER: 60/393,262  
; PRIOR FILING DATE: 2002-07-02  
; PRIOR APPLICATION NUMBER: 60/406,181  
; PRIOR FILING DATE: 2002-08-26  
; NUMBER OF SEQ ID NOS: 397  
; SOFTWARE: CuroseqList version 0.1  
; SEQ ID NO 52  
; LENGTH: 458  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-287-971-52

Query Match 100.0%; Score 117; DB 12; Length 458;  
Best Local Similarity 100.0%; Pred. No. 5.6e-10;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ORVEILEGRTECVLSNLRGRTRY 23  
|||  
Db 194 ORVEILEGRTECVLSNLRGRTRY 216

RESULT 7

US-09-016-159-5  
; Sequence 5, Application US/09016159  
; Patent No. US20020031806A1  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Jong Y  
; TITLE OF INVENTION: PURIFIED HUMAN ERYTHROPOIETIN RECEPTOR  
; TITLE OF INVENTION: PROTEIN FRAGMENT AND ANTIBODIES DERIVED THEREFROM  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C., P.A.  
; STREET: 60 South Sixth Street, Suite 3300  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM compatible

OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/016,159  
; FILING DATE: 30-JAN-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/876,227  
; FILING DATE: 16-JUN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/734,097  
; FILING DATE: 21-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/460,525  
; FILING DATE: 02-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ellinger, Mark S.  
; REGISTRATION NUMBER: 34,812  
; REFERENCE/DOCKET NUMBER: 07004/002003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612/335-5070  
; TELEFAX: 612/288-9696  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 508 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-016-159-5

Query Match 100.0%; Score 117; DB 9; Length 508;  
Best Local Similarity 100.0%; Pred. No. 6.3e-10;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ORVEILEGRTECVLSNLRGRTRY 23  
|||  
Db 194 ORVEILEGRTECVLSNLRGRTRY 216

RESULT 8

US-10-287-971-54  
; Sequence 54, Application US/10287971  
; Publication No. US20040067882A1  
; GENERAL INFORMATION:  
; APPLICANT: Alcobrook, et al  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-480A  
; CURRENT APPLICATION NUMBER: US/10/287,971  
; CURRENT FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: 09/997,425  
; PRIOR FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: 10/035,568  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: 60/338,626  
; PRIOR FILING DATE: 2001-11-05  
; PRIOR APPLICATION NUMBER: 60/401,479  
; PRIOR FILING DATE: 2002-08-06  
; PRIOR APPLICATION NUMBER: 60/333,072  
; PRIOR FILING DATE: 2001-11-06  
; PRIOR APPLICATION NUMBER: 60/348,283  
; PRIOR FILING DATE: 2001-11-09  
; PRIOR APPLICATION NUMBER: 60/393,262  
; PRIOR FILING DATE: 2002-07-02  
; PRIOR APPLICATION NUMBER: 60/406,181  
; PRIOR FILING DATE: 2002-08-26  
; SOFTWARE: CuroseqList version 0.1  
; SEQ ID NO 54  
; LENGTH: 508  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-287-971-54

Query Match 96.6%; Score 113; DB 12; Length 508;

Best Local Similarity 95.7%; Pred. No. 2.7e-09;  
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRVLEIGRTECVLSNLGRTRY 23  
|||:|||||  
Db 194 QRVKILGRTECVLSNLGRTRY 216

## RESULT 9

US-10-316-194-142  
; Sequence 142, Application US/10316194  
; Publication No. US20030215914A1  
; GENERAL INFORMATION:  
; APPLICANT: Houtzager, Erwin  
; APPLICANT: Vijjn, Irma M.C.  
; APPLICANT: Sijmons, Peter C.  
; TITLE OF INVENTION: A structure for presenting desired peptide sequences  
; FILE REFERENCE: 2183-5610US  
; CURRENT APPLICATION NUMBER: US/10/316,194  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: US 10/016,516  
; PRIOR FILING DATE: 2001-12-10  
; NUMBER OF SEQ ID NOS: 173  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 142  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: IMABIS020  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1)..(109)  
US-10-316-194-142

Query Match 88.0%; Score 103; DB 15; Length 109;  
Best Local Similarity 91.3%; Pred. No. 1.8e-08;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QRVLEIGRTECVLSNLGRTRY 23  
|||:|||||  
Db 46 QRVLEINMGRTESVLSNLGRTRY 68

## RESULT 10

US-10-316-194-144  
; Sequence 144, Application US/10316194  
; Publication No. US20030215914A1  
; GENERAL INFORMATION:  
; APPLICANT: Houtzager, Erwin  
; APPLICANT: Vijjn, Irma M.C.  
; APPLICANT: Sijmons, Peter C.  
; TITLE OF INVENTION: A structure for presenting desired peptide sequences  
; FILE REFERENCE: 2183-5610US  
; CURRENT APPLICATION NUMBER: US/10/316,194  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: US 10/016,516  
; PRIOR FILING DATE: 2001-12-10  
; NUMBER OF SEQ ID NOS: 173  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 144  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: IMABIS027  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1)..(109)  
US-10-316-194-144

Query Match 82.1%; Score 96; DB 15; Length 109;  
Best Local Similarity 87.0%; Pred. No. 2.3e-07;

Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QRVLEIGRTECVLSNLGRTRY 23  
|||:|||||  
Db 46 QRVLEINMGRTESVLSNLGRTRY 68

## RESULT 11

US-10-316-194-35  
; Sequence 35, Application US/10316194  
; Publication No. US20030215914A1  
; GENERAL INFORMATION:  
; APPLICANT: Houtzager, Erwin  
; APPLICANT: Vijjn, Irma M.C.  
; APPLICANT: Sijmons, Peter C.  
; TITLE OF INVENTION: A structure for presenting desired peptide sequences  
; FILE REFERENCE: 2183-5610US  
; CURRENT APPLICATION NUMBER: US/10/316,194  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: US 10/016,516  
; PRIOR FILING DATE: 2001-12-10  
; NUMBER OF SEQ ID NOS: 173  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 35  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: VAP amino acid  
; FEATURE:  
; OTHER INFORMATION: sequence of Imab600  
; NAME/KEY: SITE  
; LOCATION: (1)..(109)  
US-10-316-194-35

Query Match 79.5%; Score 93; DB 15; Length 109;  
Best Local Similarity 87.0%; Pred. No. 6.7e-07;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QRVLEIGRTECVLSNLGRTRY 23  
|||:|||||  
Db 46 QRVLEINMGRTESVLSNLGRTRY 68

## RESULT 12

US-10-316-194-43  
; Sequence 43, Application US/10316194  
; Publication No. US20030215914A1  
; GENERAL INFORMATION:  
; APPLICANT: Houtzager, Erwin  
; APPLICANT: Vijjn, Irma M.C.  
; APPLICANT: Sijmons, Peter C.  
; TITLE OF INVENTION: A structure for presenting desired peptide sequences  
; FILE REFERENCE: 2183-5610US  
; CURRENT APPLICATION NUMBER: US/10/316,194  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: US 10/016,516  
; PRIOR FILING DATE: 2001-12-10  
; NUMBER OF SEQ ID NOS: 173  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 43  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: VAP amino acid  
; FEATURE:  
; OTHER INFORMATION: sequence of Imab1100  
; NAME/KEY: SITE  
; LOCATION: (1)..(109)  
US-10-316-194-43

Query Match 73.5%; Score 86; DB 15; Length 109;



Best Local Similarity 82.6%; Pred. No. 8.6e-06;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 QRVETLGRTECVLSNLRGRTRY 23

Db 46 QRVETLGRTECVLSNLRGRTRY 68

RESULT 13

US-09-947-063-4  
; Sequence 4, Application US/09947063  
; Publication No. US20030059775A1  
; GENERAL INFORMATION:

; APPLICANT: Padigaru et al.

; TITLE OF INVENTION: No. US20030059775A1e1 Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-112

; CURRENT APPLICATION NUMBER: US/09/947,063

; PRIOR FILING DATE: 2001-09-05

; PRIOR APPLICATION NUMBER: 60/229,990

; PRIOR FILING DATE: 2000-09-05

; PRIOR APPLICATION NUMBER: 60/229,988

; PRIOR FILING DATE: 2000-09-05

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 1026

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-947-063-4

Query Match 44.4%; Score 52; DB 10; Length 1026;  
Best Local Similarity 71.4%; Pred. No. 27;

Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 EGRTECVLSNLRGR 20

Db 292 EGRTECVLSNLRGR 305

RESULT 14

US-09-947-063-11

; Sequence 11, Application US/09947063

; Publication No. US20030059775A1

; GENERAL INFORMATION:

; APPLICANT: Padigaru et al.

; TITLE OF INVENTION: No. US20030059775A1e1 Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-112

; CURRENT APPLICATION NUMBER: US/09/947,063

; PRIOR FILING DATE: 2001-09-05

; PRIOR APPLICATION NUMBER: 60/229,990

; PRIOR FILING DATE: 2000-09-05

; PRIOR APPLICATION NUMBER: 60/229,988

; PRIOR FILING DATE: 2000-09-05

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 11

; LENGTH: 1026

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-947-063-11

Query Match 44.4%; Score 52; DB 10; Length 1026;  
Best Local Similarity 71.4%; Pred. No. 27;

Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 EGRTECVLSNLRGR 20

Db 292 EGRTECVLSNLRGR 305

RESULT 15

US-09-728-912-7

; Sequence 7, Application US/09728912

; Patent No. US20010036643A1

; GENERAL INFORMATION:

; APPLICANT: Holloway, James L.

; TITLE OF INVENTION: Tumor Necrosis Factor-Stimulated Gene

; FILE REFERENCE: 99-94US

; CURRENT APPLICATION NUMBER: US/09/728,912

; PRIOR FILING DATE: 2000-12-01

; PRIOR APPLICATION NUMBER: 60/169,252

; PRIOR FILING DATE: 1999-12-06

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 7

; LENGTH: 49

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-728-912-7

Query Match 41.9%; Score 49; DB 9; Length 49;  
Best Local Similarity 50.0%; Pred. No. 2.4;

Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 3 VEILGRTECVLSNLRGRTR 22

Db 7 VELLDDGYTHRVLARFHGRSR 26

Search completed: May 6, 2004, 12:48:22  
Job time : 43 secs

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